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**FIG. 1**

<i>Bet v 1</i> sense	5' - AATTATGAGACTGAGACCA <u>C</u> CTCTGTTATCCCAGCAGCTCG	-3'
<i>Bet v 1</i> non-sense	3' - TTAATACTCTGACTCTGGTGGAGACAATAGGGTCGTCGAGC	-5'
sense primer	5' - TGAGACCC <u>C</u> CTCTGTTATCCCAG	-3'
non-sense primer	3' - ATACTCTGACTCTGGGGGAGACA	-5'

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## FIG. 2

all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4: 186Bv, 31-mer 5'-GATACCCTCTTTCCACAGGTTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTTTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTTCCTGAAATGTTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA
4	non-sense	9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCATGCAAACCTTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGCATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTTCCCTCAGGCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

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## FIG. 3

1 (A-C)

GGTGTGTTTAATTATGAGACTGAGACCACTCTGTTATCCCAGCAGCTCGACTGTTCAAG 60  
G V F N Y E T E T T P S V I P A A R L F K 20

9 (A-G) 2 (A-C) 2 (A-C)

GCCTTTATCCTTGATGGCGATAACCTCTTTCCAAGGTTGCACCCCAAGCCATTAGCAGT 120  
A F I L D G G D N T L F P K Q V A P Q A I S S 40

3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 (GA-TC)

GTGAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAGAAGATCAGCTTTCCCGAA 180  
V E N I E S G N S G G P G T I K K N I S F P E S 60

5 (CA-TG)

GGCCTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGGACCACACAAACTTCAAA 240  
G L P F K Y V K D R V D E V D H T A N F K 80

TACAATTACAGCGTGATCGAGGGCGGTCCCATAGGCGACACATTGGAGAAGATCTCCAAC 300  
Y N Y S V I E G G P I G D T L E K I S N 100

10 (GAG-CAC) 8 (CCC-TGG)

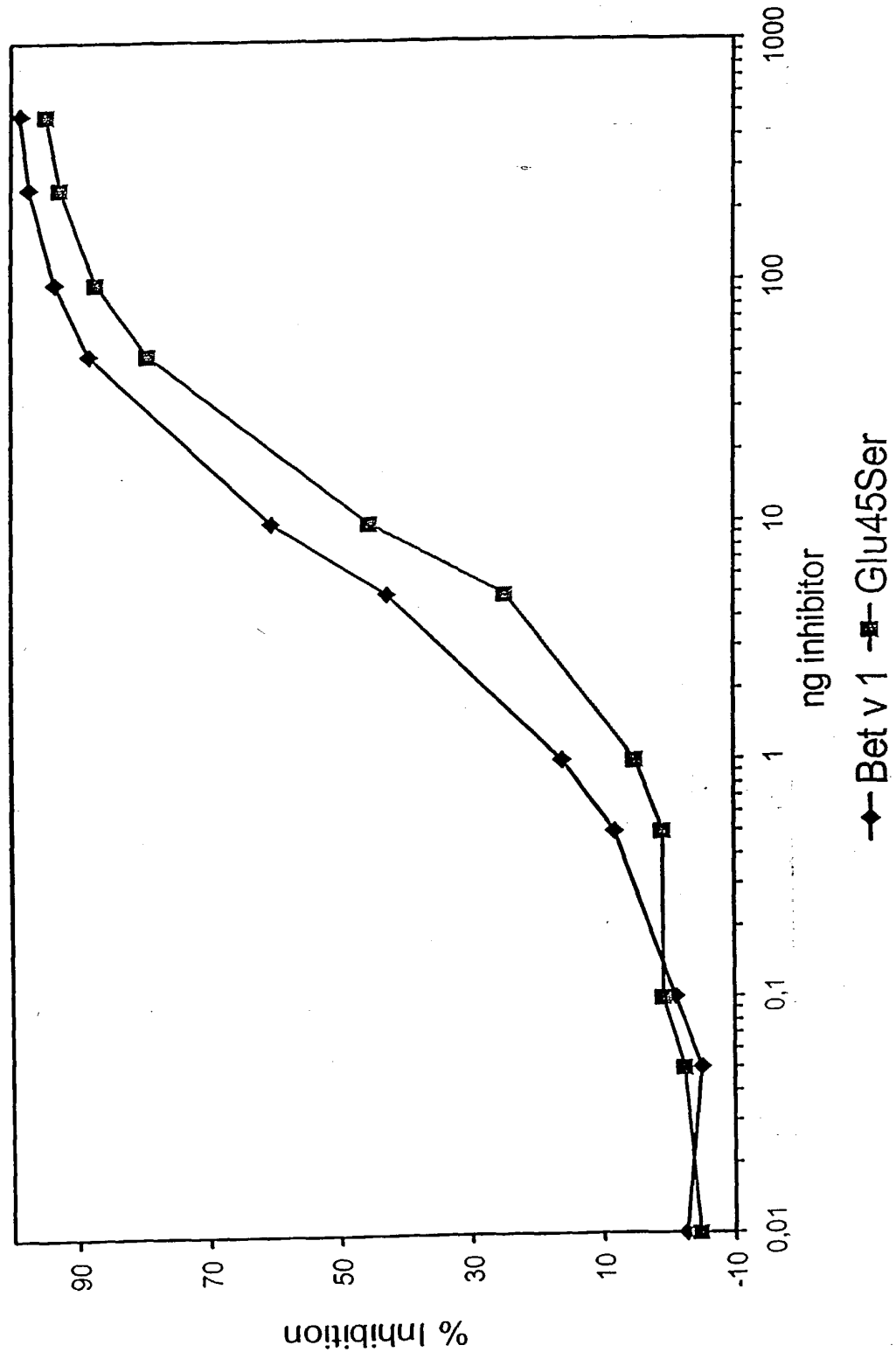
GAGATAAAGATAGTGGCAACCCCTGATGGAGGATCCATCTTGAAGATCAGCAACAAGTAC 360  
E I K I V A T P G D G G S I L K I S N K Y 120

CACACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTTAAGGCAAGTAAGAAATGGGC 420  
H T K G D H E V K A E Q V K A S K E M G 140

GAGACACTTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCTACAACATA 480  
E T L L R A V E S Y L L A H S D A Y N stop 159



FIG. 4

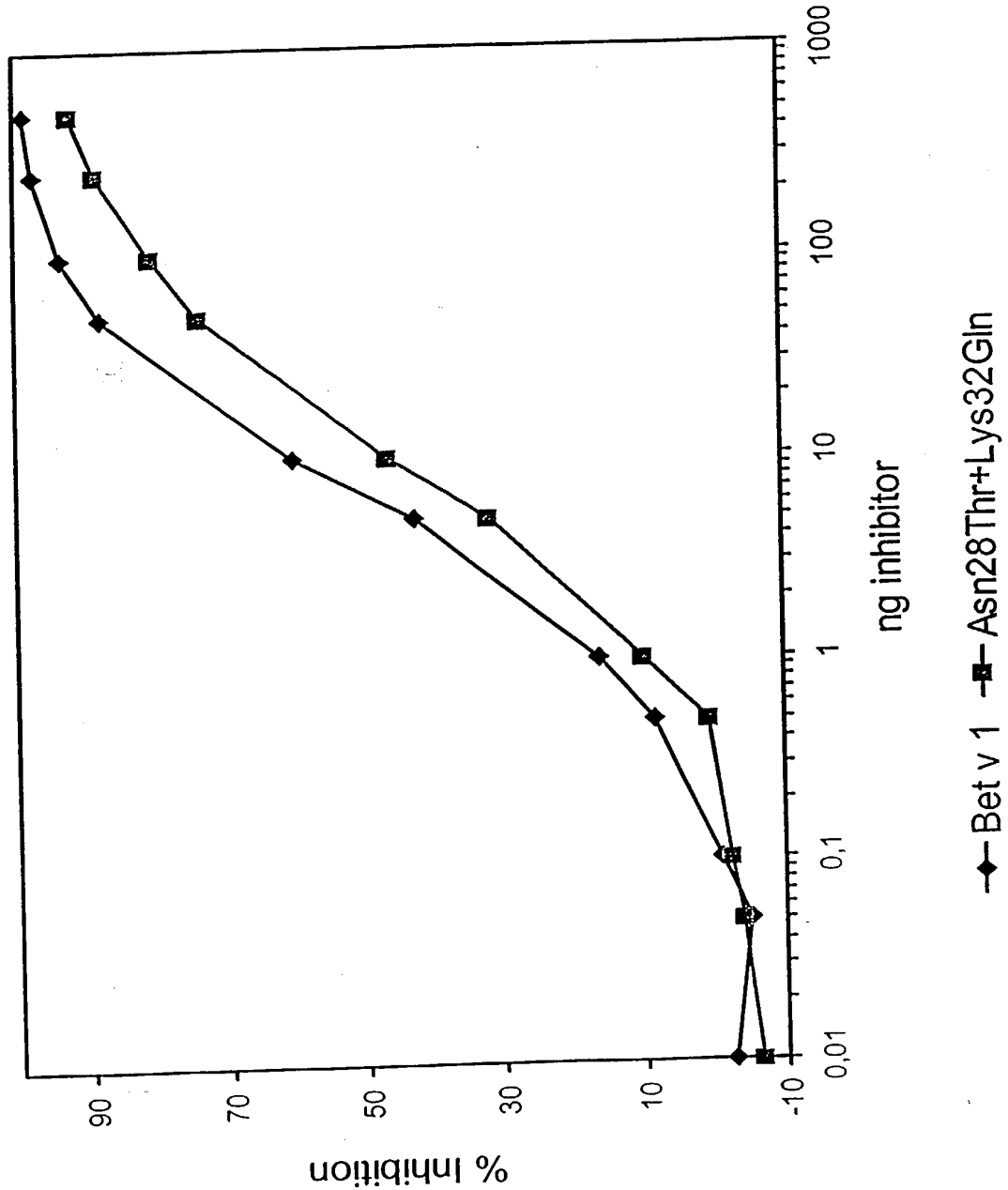


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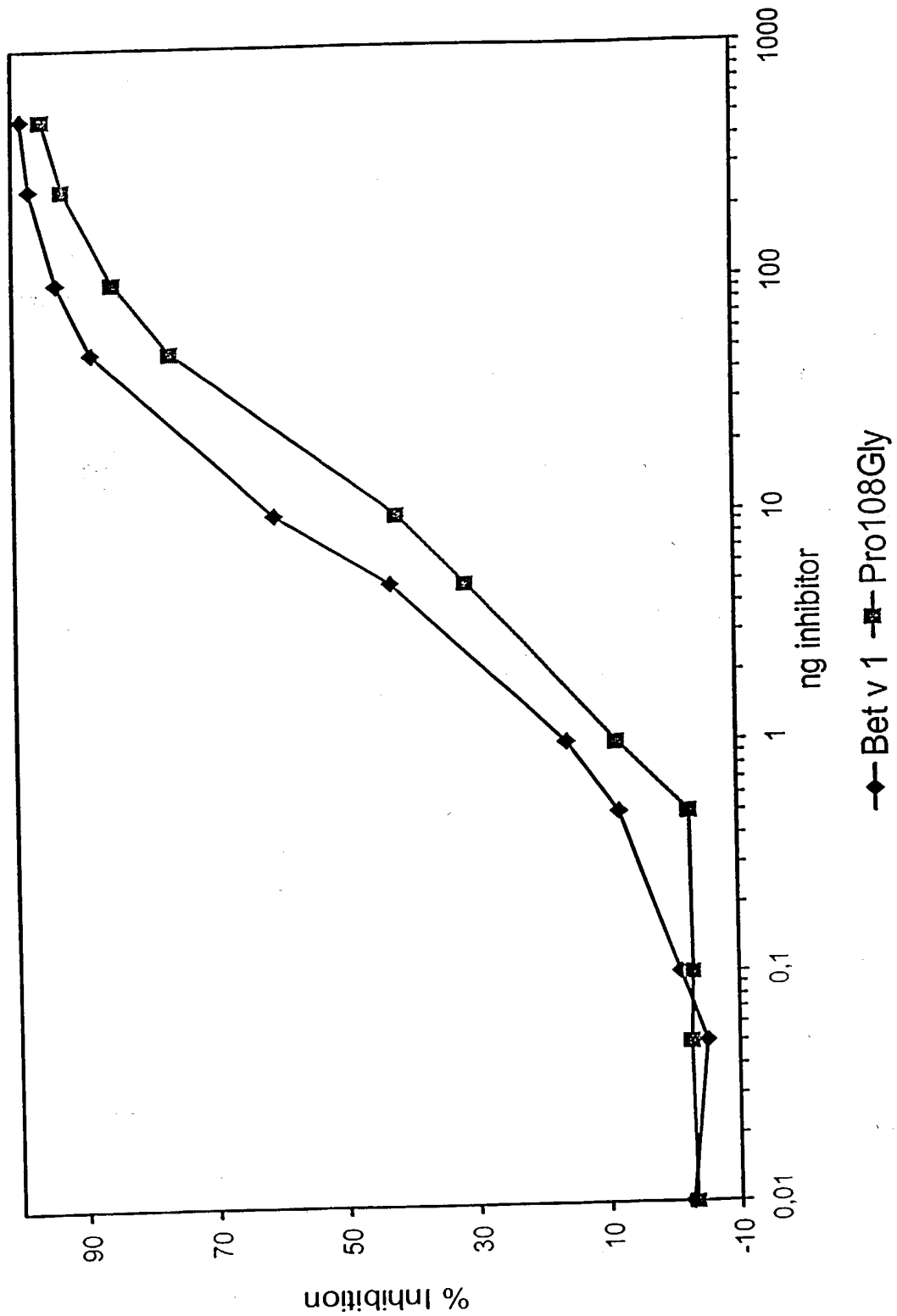
FIG. 5



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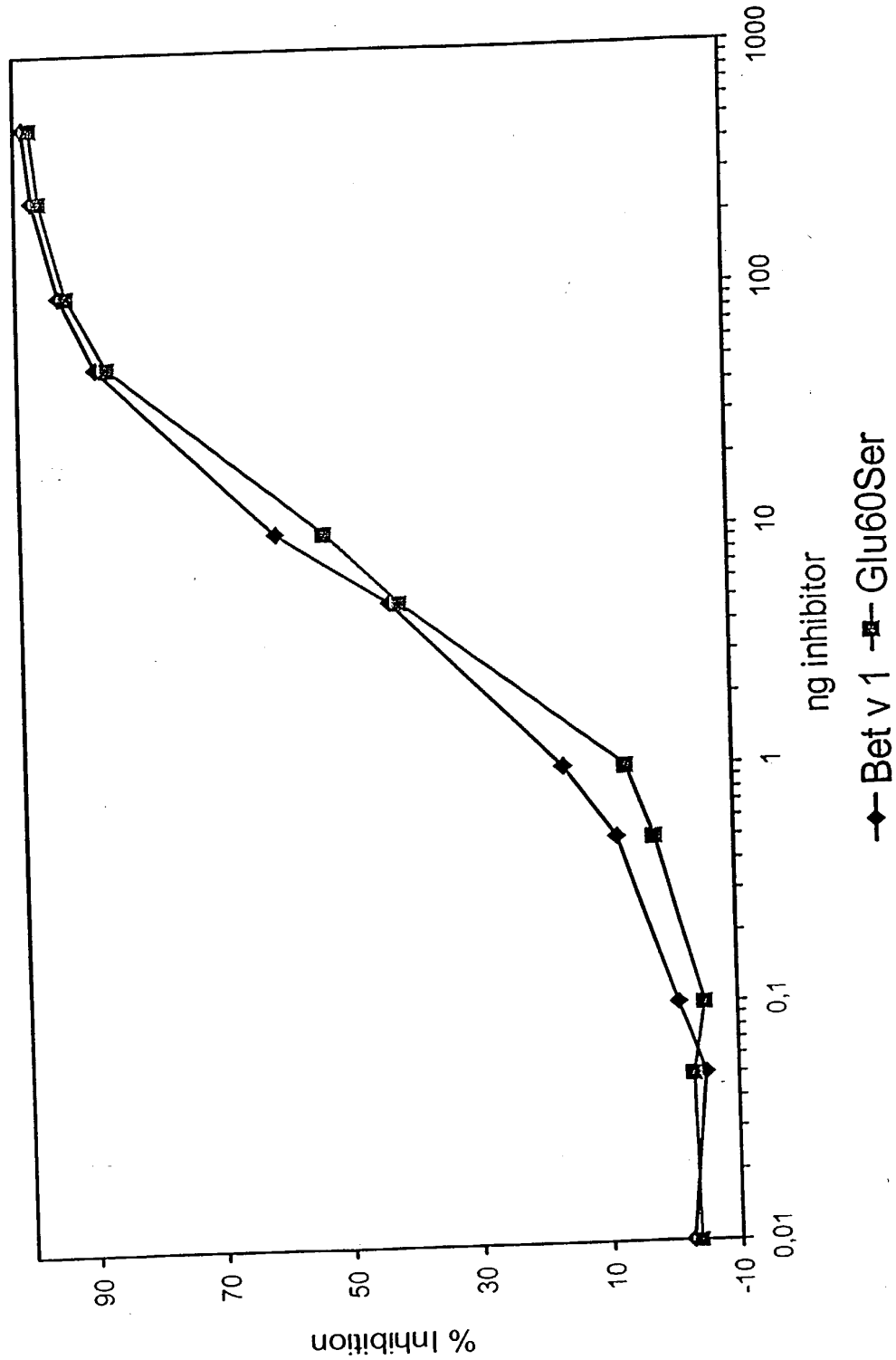


FIG. 6





**FIG. 7**




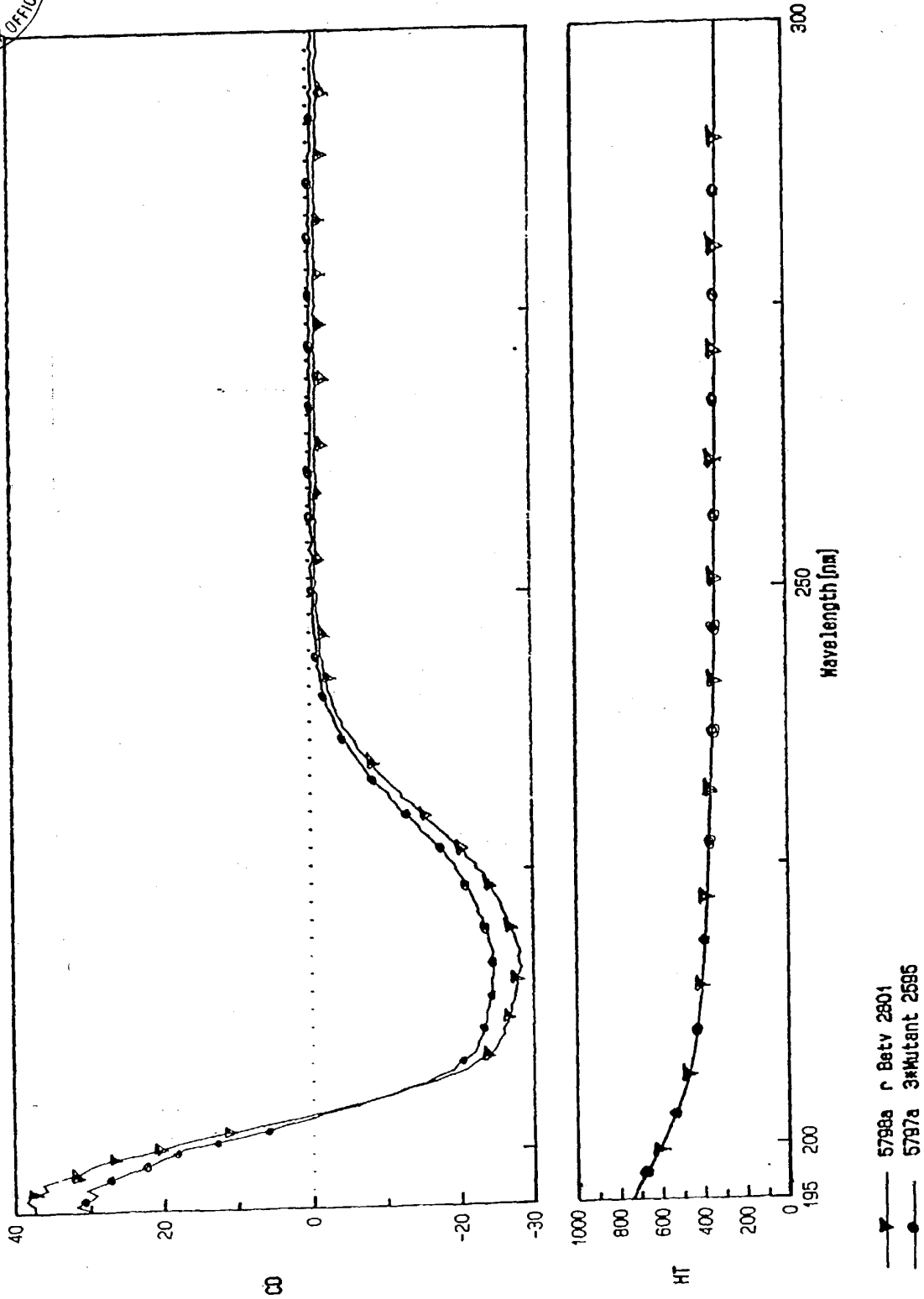
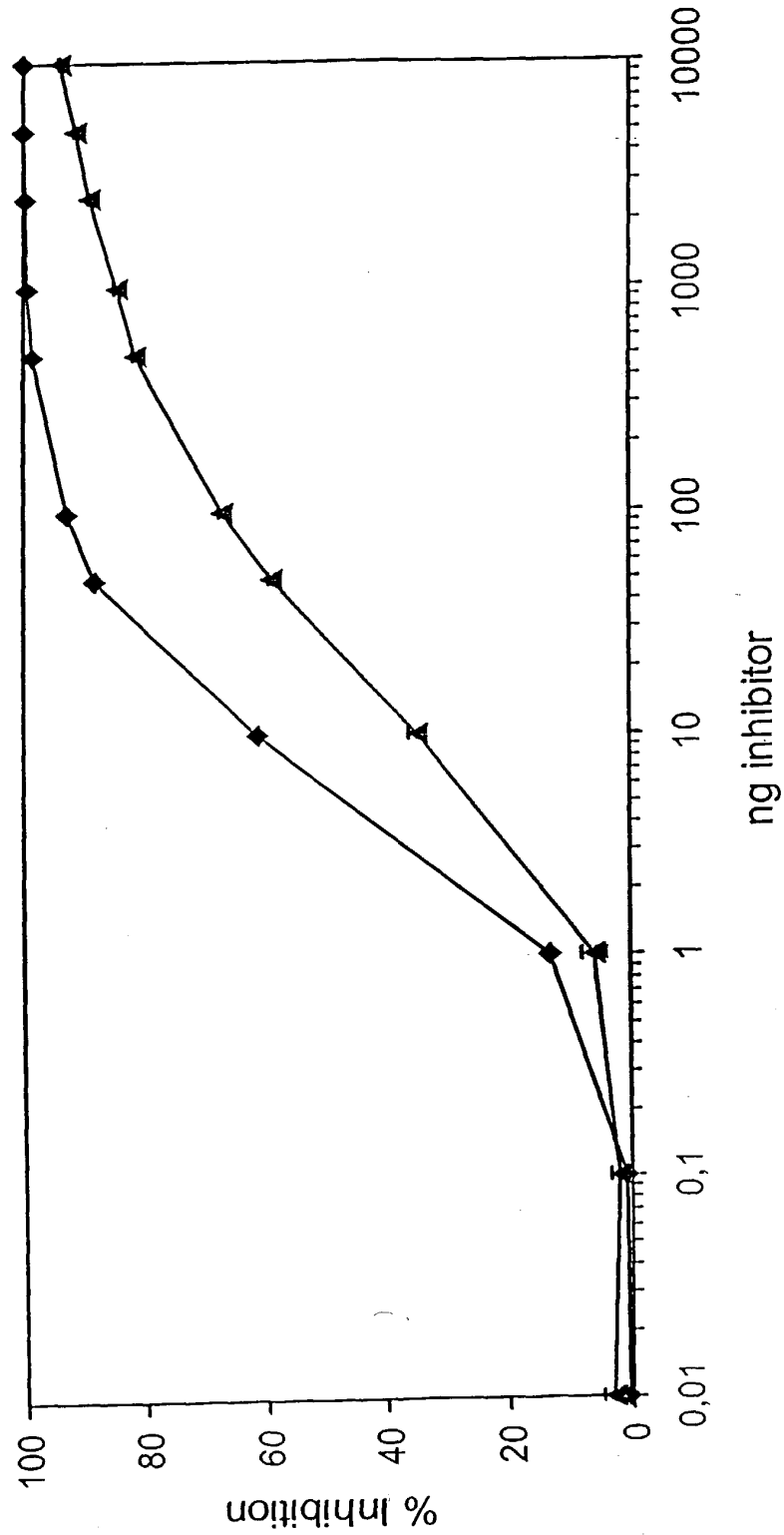
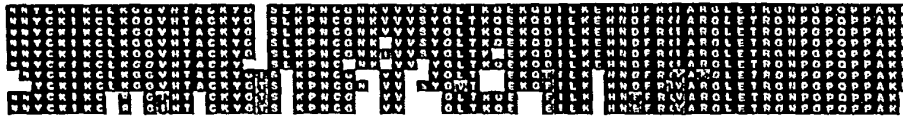


FIG. 8





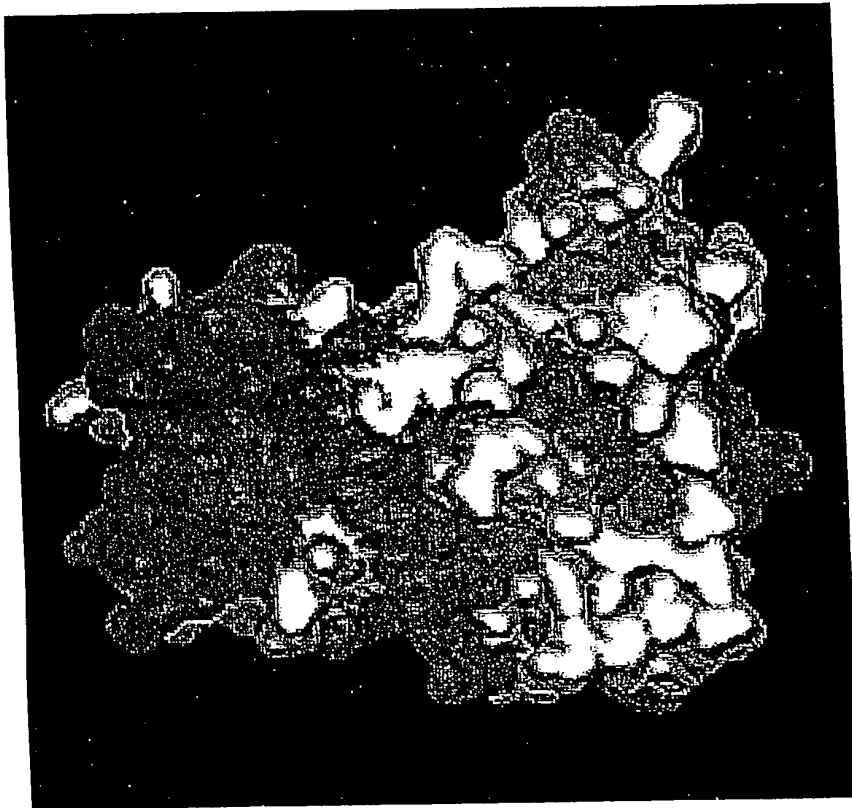
**FIG. 9**



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**FIG. 10 B**



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## FIG. 11 A

Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5'-	ACCACAGCCTCCAGCGAAGAATATGAAAAATTGGTATGGA	-3'
Ves v 5 non-sense	3'-	TGGTGTCTGGAGGTCGCTTCTTATACTTTTAAACCATACCT	-5'
sense primer	5'-	CCAGCGGCTAATATGAAAAAT	-3'
non-sense primer	3'-	GTCGGAGGTCGCCGATTATAC	-5'

## FIG. 11 B

Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5'-	GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG	-3'
Ves v 5 non-sense	3'-	CCGATTAGTTACAGTTATACCAGTGCTATGAACGTCCCTAC	-5'
sense primer	5'-	TGTCAAGCTGGTCACGATACT	-3'
non-sense primer	3'-	TTAGTTACAGTTCCGACCAGTG	-5'

## FIG. 12

all sense 1: XhoI start, 38-mer:

EcoRI  
 5'-CCGCTCGAGAAAAGAAACAATTATTGTAAAATAAAATG  
 L E K R N N Y C K I K  
 Kex2 cleavage site amino terminus of Ves v 5

1 sense	1: K72As	21-mer	5'-CCAGCGGCTAATATGAAAAAT
1 non-sense	2: K72Aa	21-mer	5'-CATATTAGCCGCTGGAGGCTG
2 sense	3: Y96As	21-mer	5'-TGTCAAGCTGGTCACGATACT
2 non-sense	4: Y96Aa	21-mer	5'-GTGACCAGCTTGACATTGATT
all non-sense	7: CT-pPICZαA,	21-mer	5'-ATTCATCAGCTGCGAGATAGG

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# FIG. 13

1	AACAATTATTGTAAAATAAAATGTTTGAAAGGAGGTGTCCATACTGCCTGCAAATATGGA	60
1	N N Y C K I K C L K G G V H T A C K Y G	20
61	AGTCTTAAACCGAATTGCGGTAATAAGGTAGTGGTATCCTATGGTCTAACGAAACAAGAG	120
21	S L K P N C G N K V V V S Y G L T K Q E	40
121	AAACAAGACATCTTAAAGGAGCACAATGACTTTAGACAAAAAATTGCACGAGGATTGGAG	180
41	K Q D I L K E H N D F R Q K I A R G L E	60
	1 [K72A] (AAG-GCT)	
181	ACTAGAGGTAATCCTGGACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGAAC	240
61	T R G N P G P Q P P A K N M K N L V W N	80
	2 [Y96A] (TA-GC)	
241	GACGAGTTAGCTTATGTGCGCCCAAGTGTGGGCTAATCAATGTCAATATGGTCACGATACT	300
81	D E L A Y V A Q V W A N Q C Q Y G H D T	100
301	TGCAGGGATGTAGCAAAATATCAGGTTGGACAAAACGTAGCCTTAACAGGTAGCACGGCT	360
101	C R D V A K Y Q V G Q N V A L T G S T A	120
361	GCTAAATACGATGATCCAGTTAAACTAGTTAAATGTGGGAAGATGAAGTGAAAGATTAT	420
121	A K Y D D P V K L V K M W E D E V K D Y	140
421	AATCCTAAGAAAAAGTTTTCGGGAAACGACTTTCTGAAAACCGGCCATTACACTCAAATG	480
141	N P K K K F S G N D F L K T G H Y T Q M	160
481	GTTTGGGCTAACACCAAGGAAGTTGGTTGTGGAAGTATAAAATACATTCAAGAGAAATGG	540
161	V W A N T K E V G C G S I K Y I Q E K W	180
541	CACAAACATTACCTTGTATGTAATTATGGACCCAGCGGAAACTTTAAGAATGAGGAACTT	600
181	H K H Y L V C N Y G P S G N F K N E E L	200
601	TATCAAACAAAGTAA	612
201	Y Q T K stop	204



FIG. 14

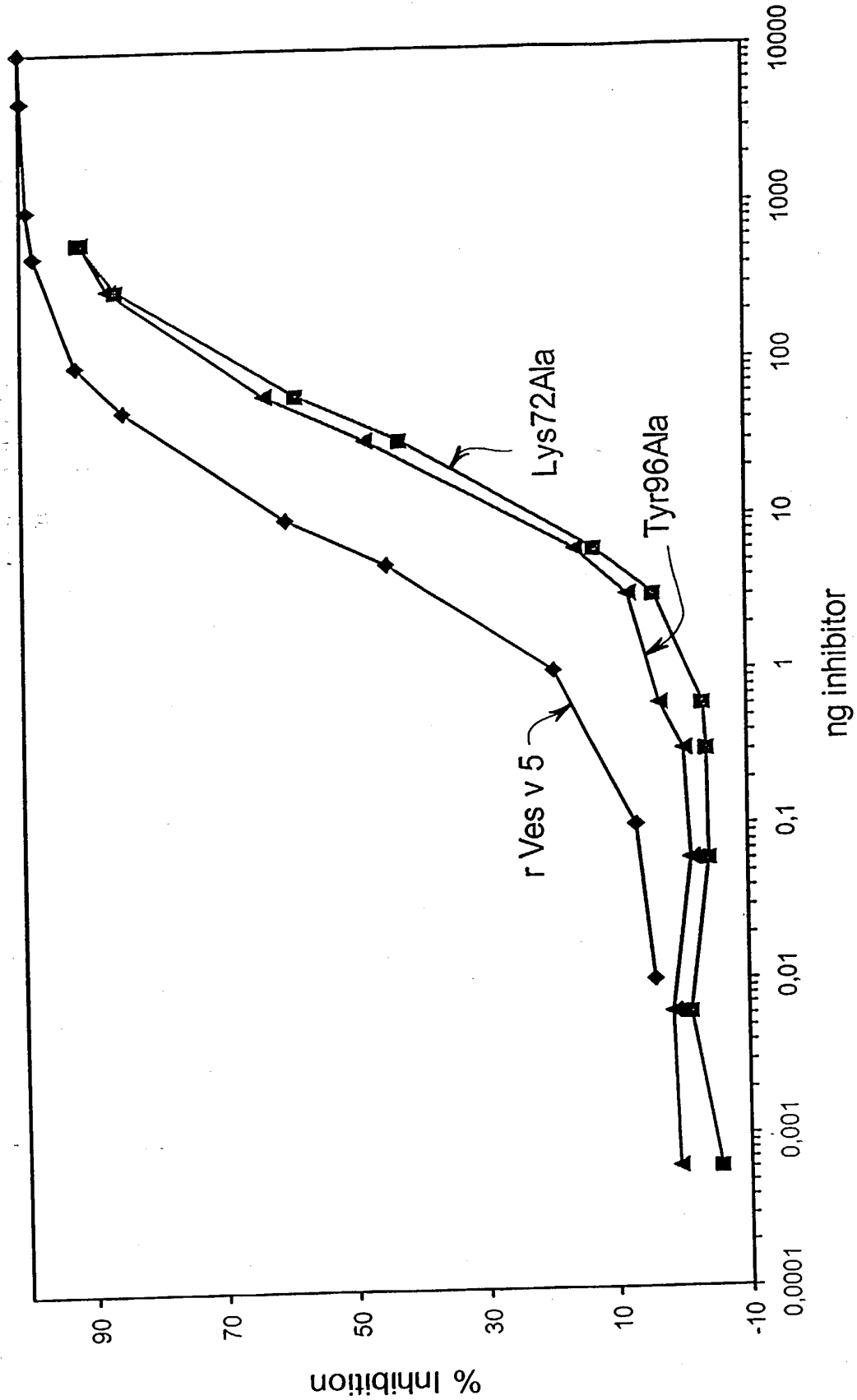
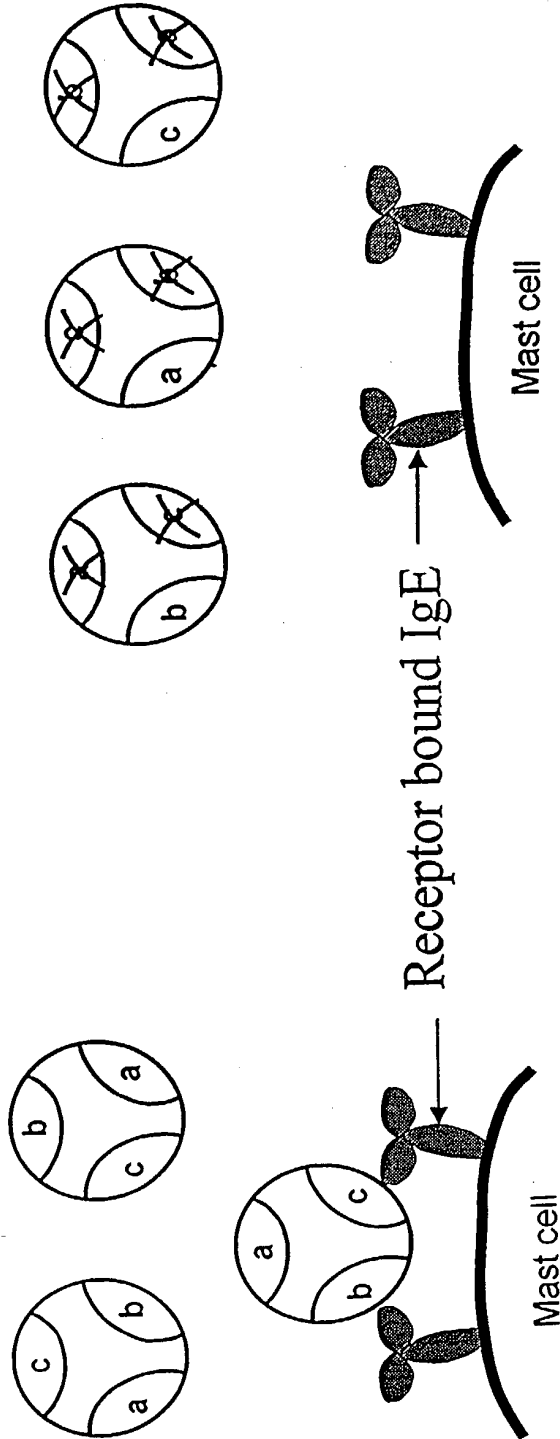




FIG. 15 B

FIG. 15 A



No cross-linking

Cross-linking



## FIG. 16 A

### DNA SEQUENCE

#### ORIGIN

```

1      cacaaattct tcttcttcc ttactactga tcattaatct gaaaacaaaa ccaaacaac
61     cattcaaaat gatgtacaaa atttgtgtc ttcatgtt ggtcgagcc gttgctgtg
121    atcaagtga tgtcaaagat tgtgccaatc atgaaatcaa aaaagtttg gtaccaggat
181    gccatggtc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccggtt
241    tcgaagccaa ccaaaacaca aaaacggcta aaattgaaat caaagcctca atcgatggtt
301    tagaagtga tgttcccggt atcgatccaa atgcatgcc ttacatgaaa tgcccattgg
361    ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcaccaaatt
421    ctgaaaatgt tgcgtcact gttaaagta tgggtgatga tgggttttg gcctgtgcta
481    ttgtactca tgctaaaatc cgcgattaaa tcaaacaaaa ttattgatt ttgtaatcac
541    aatgattga ttttcttcc aaaaaaaaaa taaataaaat ttgggaatt c

```

## FIG. 16 B

```

1      mmykilclsl lvaavardqv dvkdcanhei kkvlvpgchg sepciihrk pfqleavfea
61     nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen
121    vvvtkvmgd dgvlaciat hakird

```



(I) X30Y  
 (1) (2) X50Y  
 (3) (4) X70Y  
 (5) (6) X90Y  
 (7) (8) X110Y  
 (9) (10)  
 (11) (12)

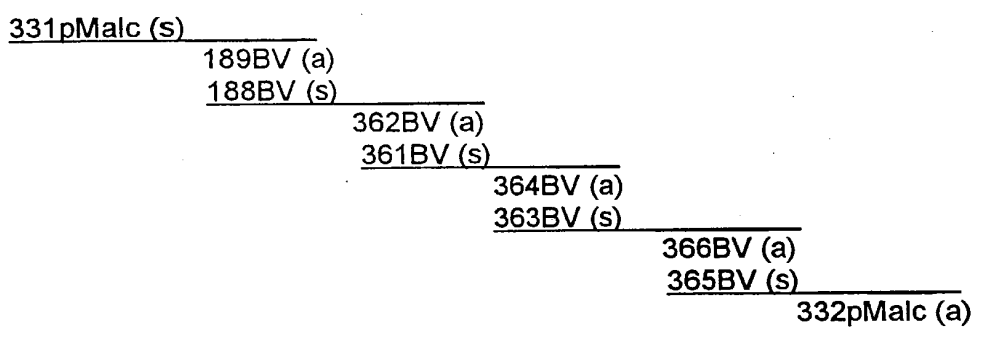
(II) X30Y X50Y X70Y X90Y X110Y  
 (1) (2)





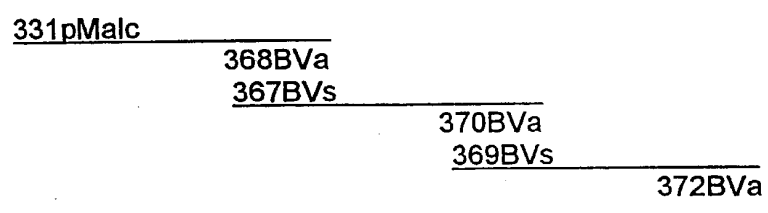
# FIG. 18 A

DNA template: Bet v 1 (2589) carrying the Y5V mutation.



# FIG. 18 B

DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations.

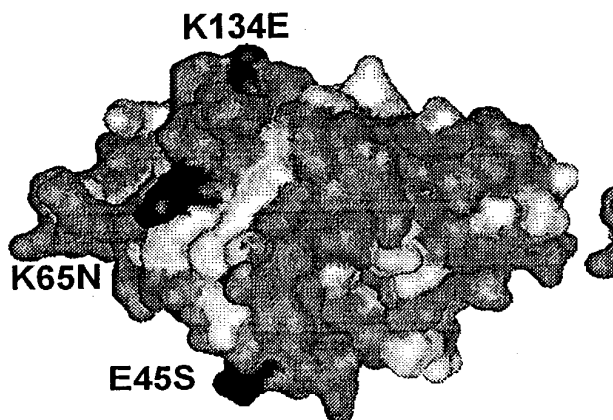
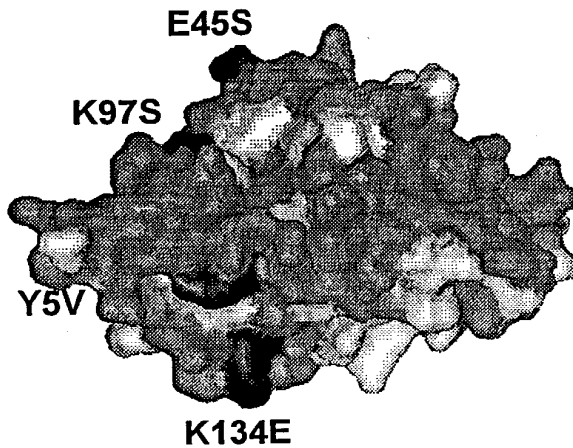
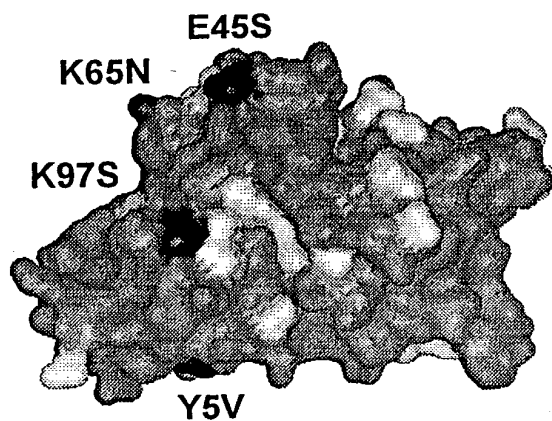


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# FIG. 19 A

Bet v 1 (2628)

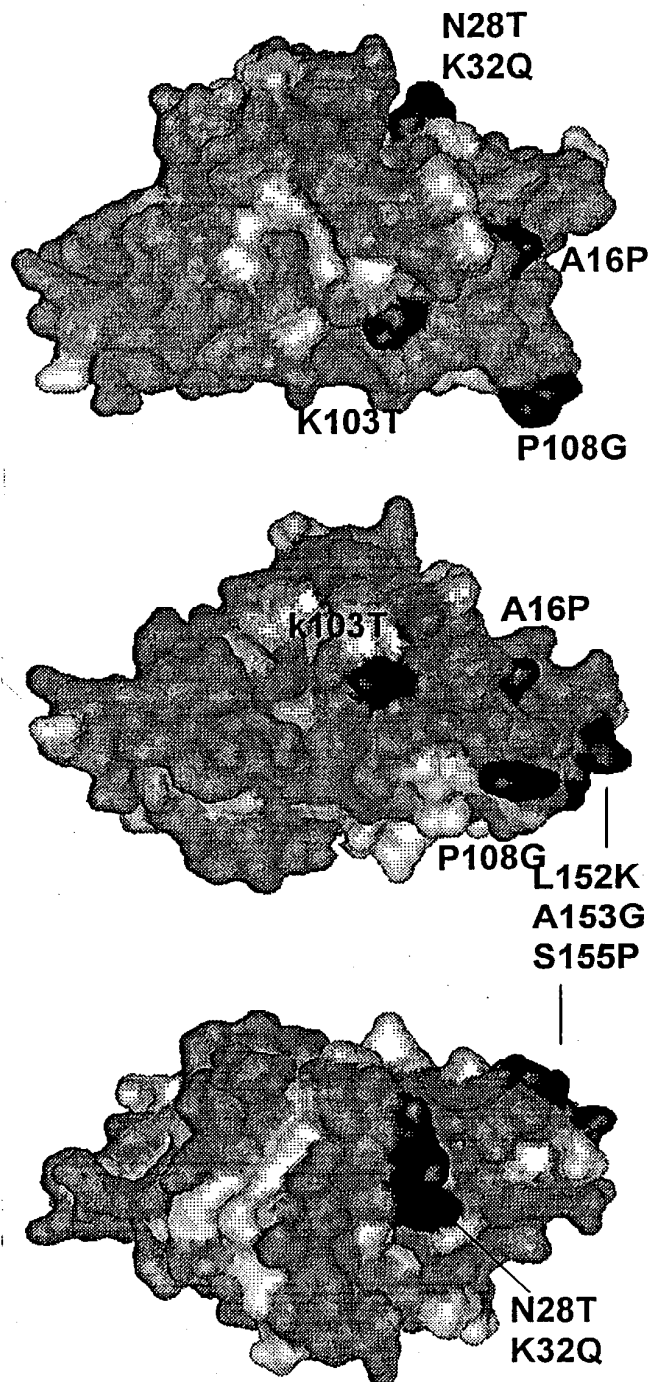


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## FIG. 19 B

Bet v 1 (2637)



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FIG. 20

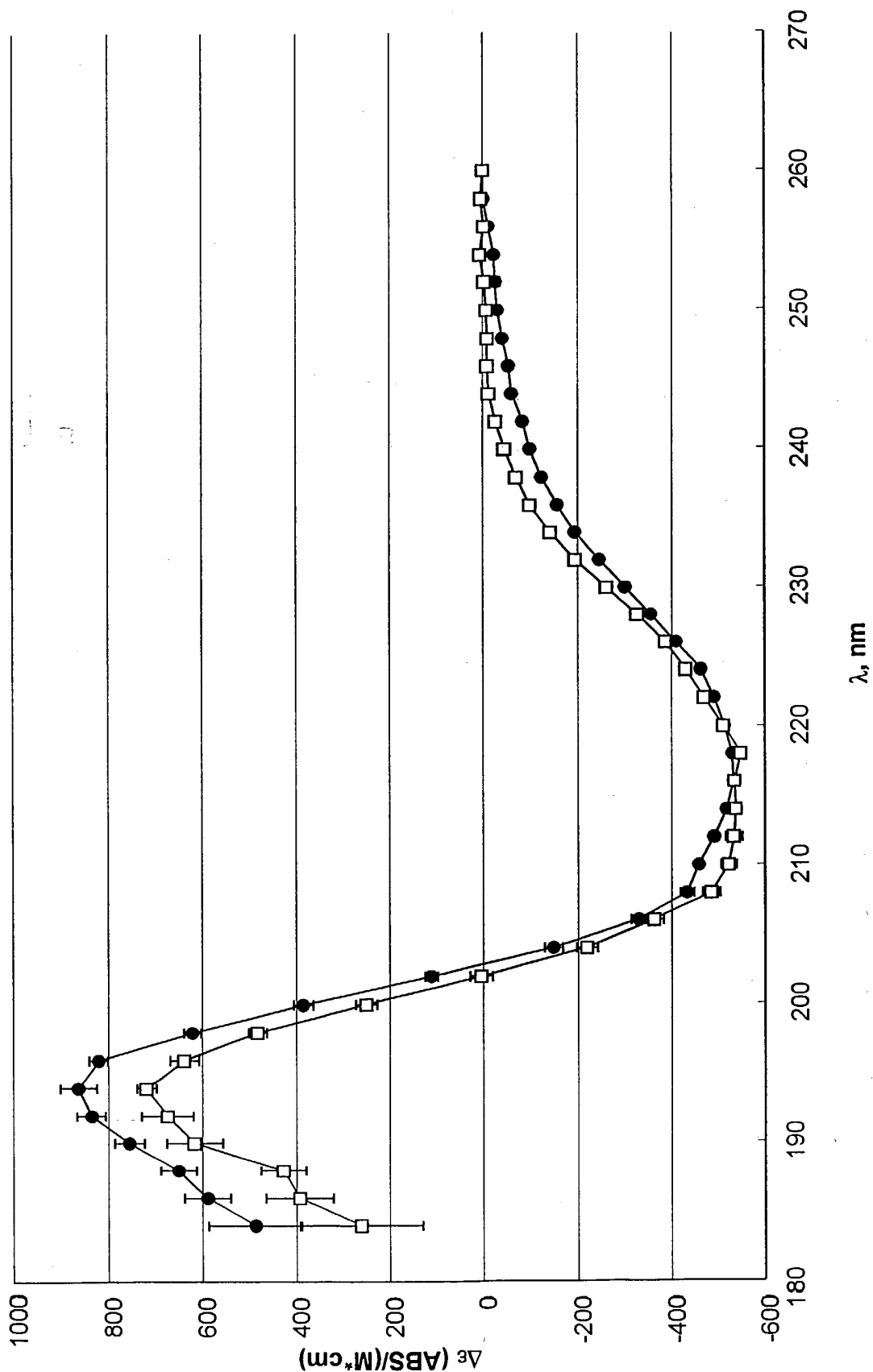
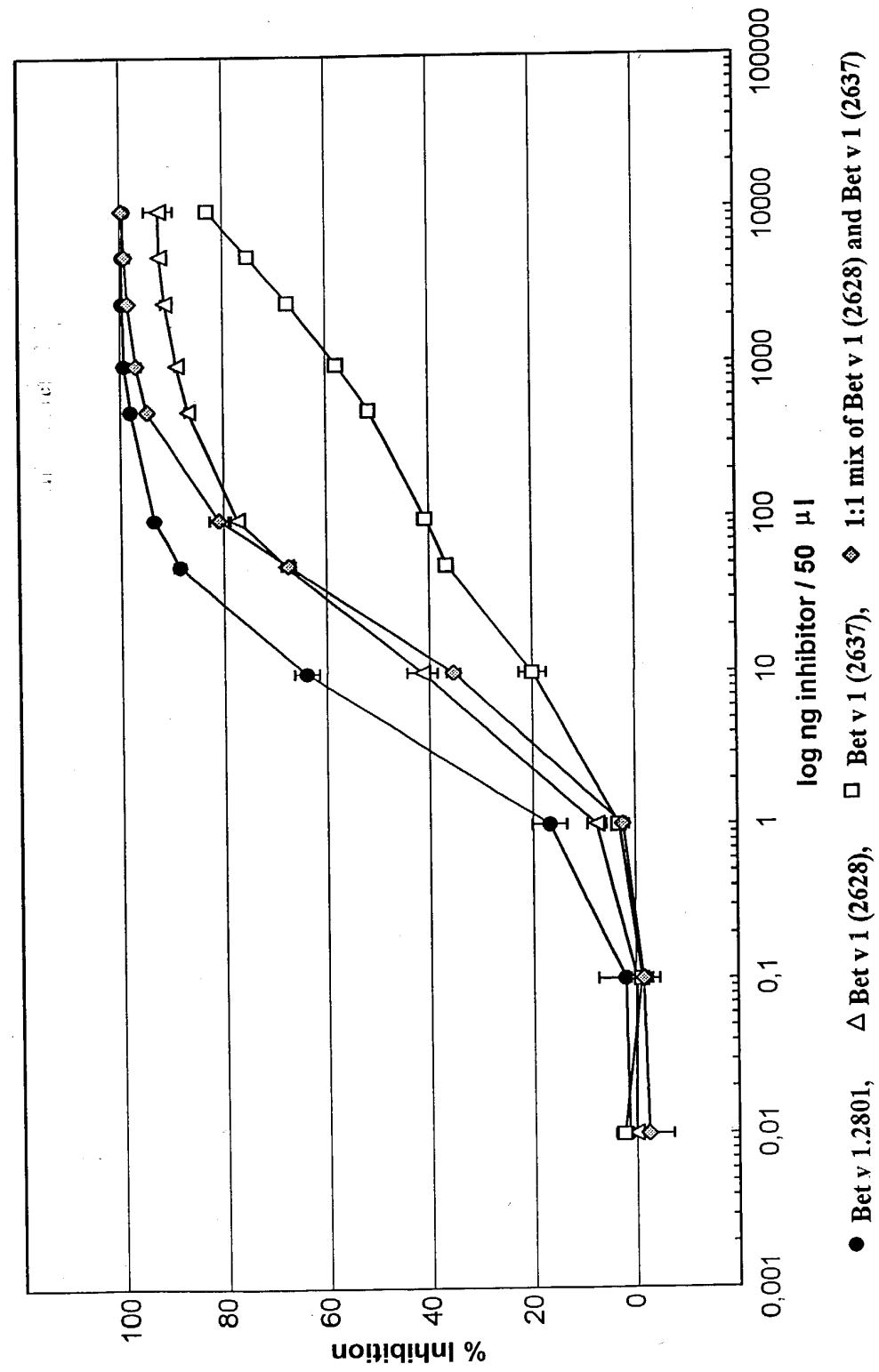




FIG. 21



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FIG. 22

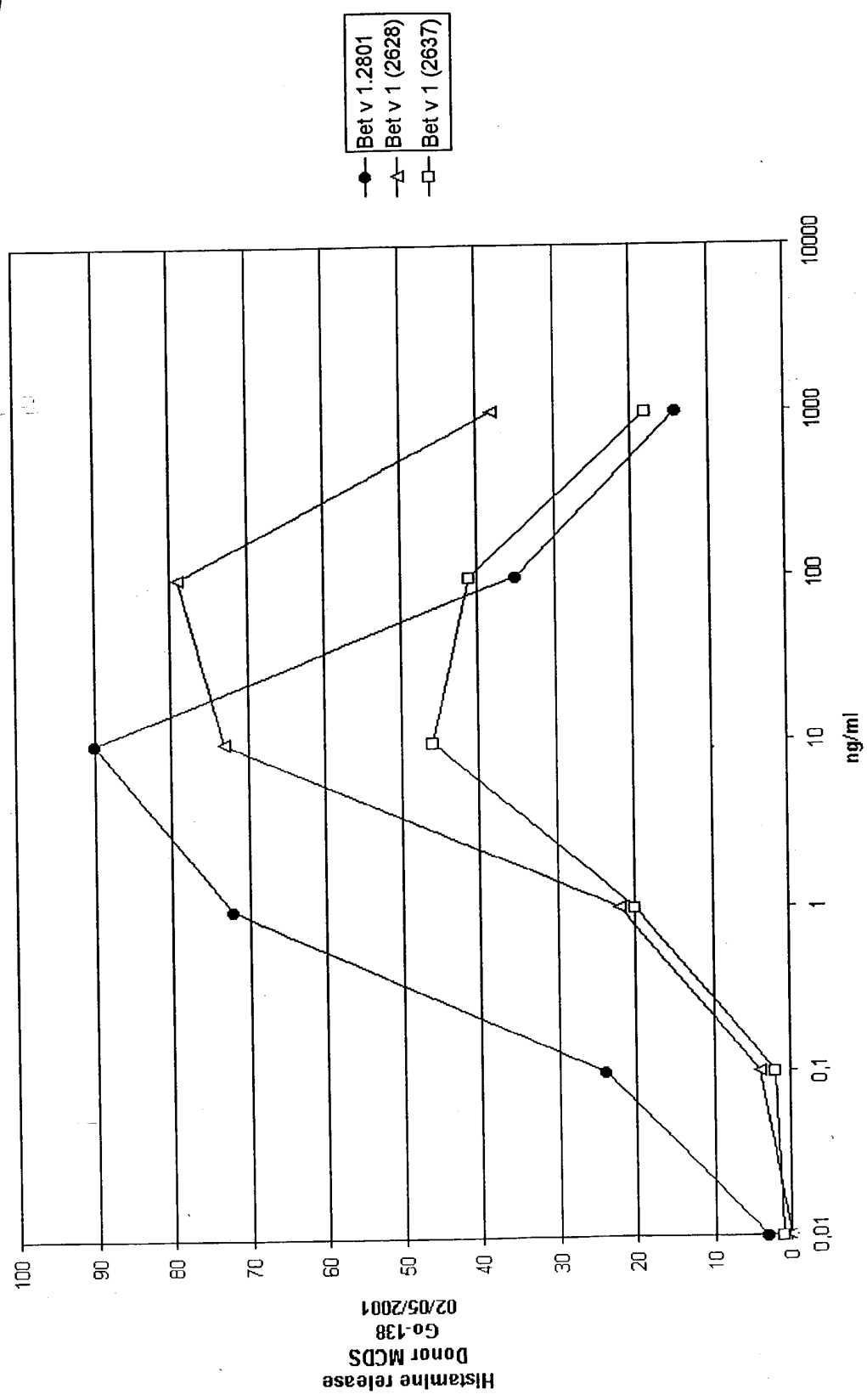
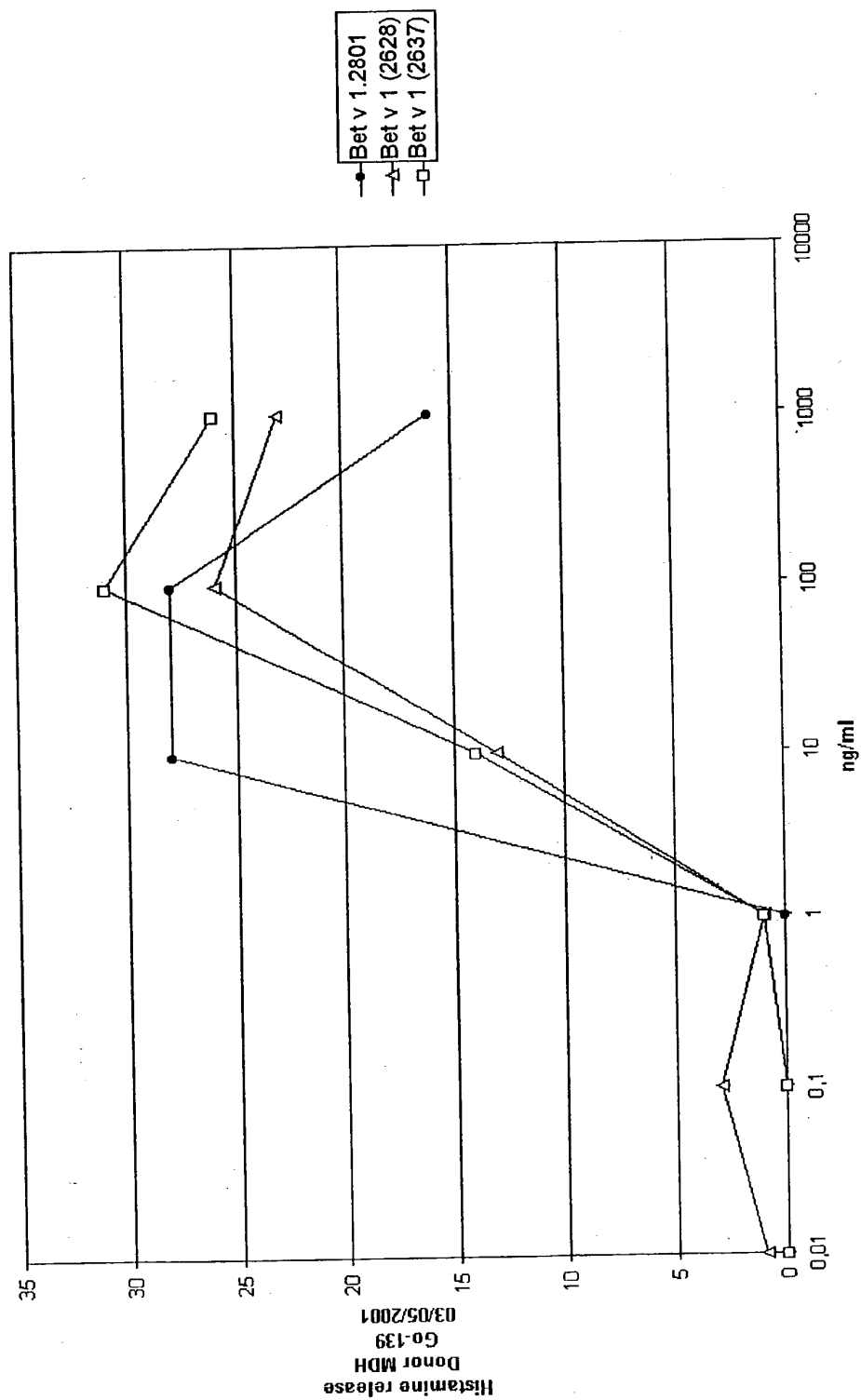


FIG. 23



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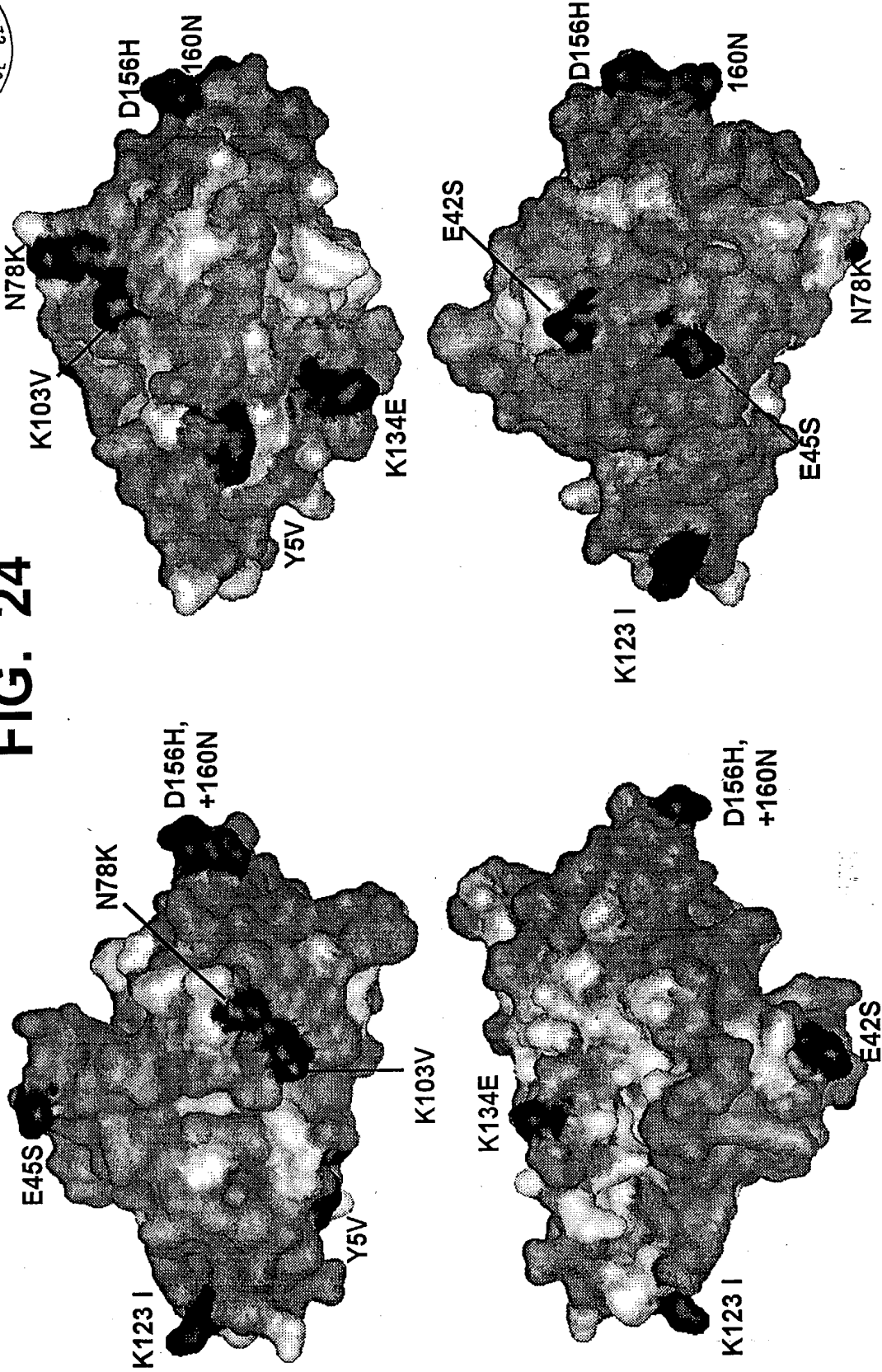
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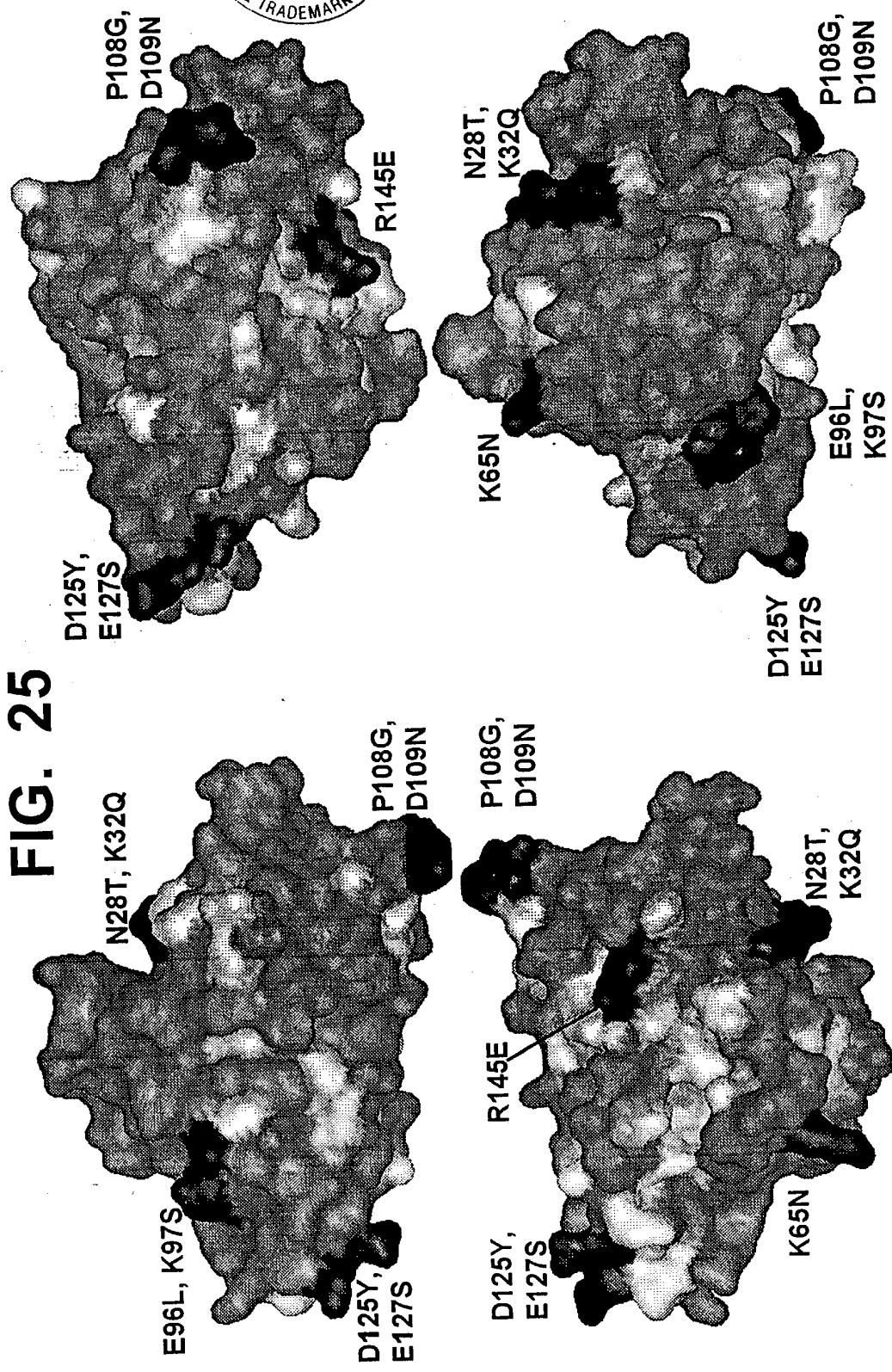
FIG. 24





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FIG. 25



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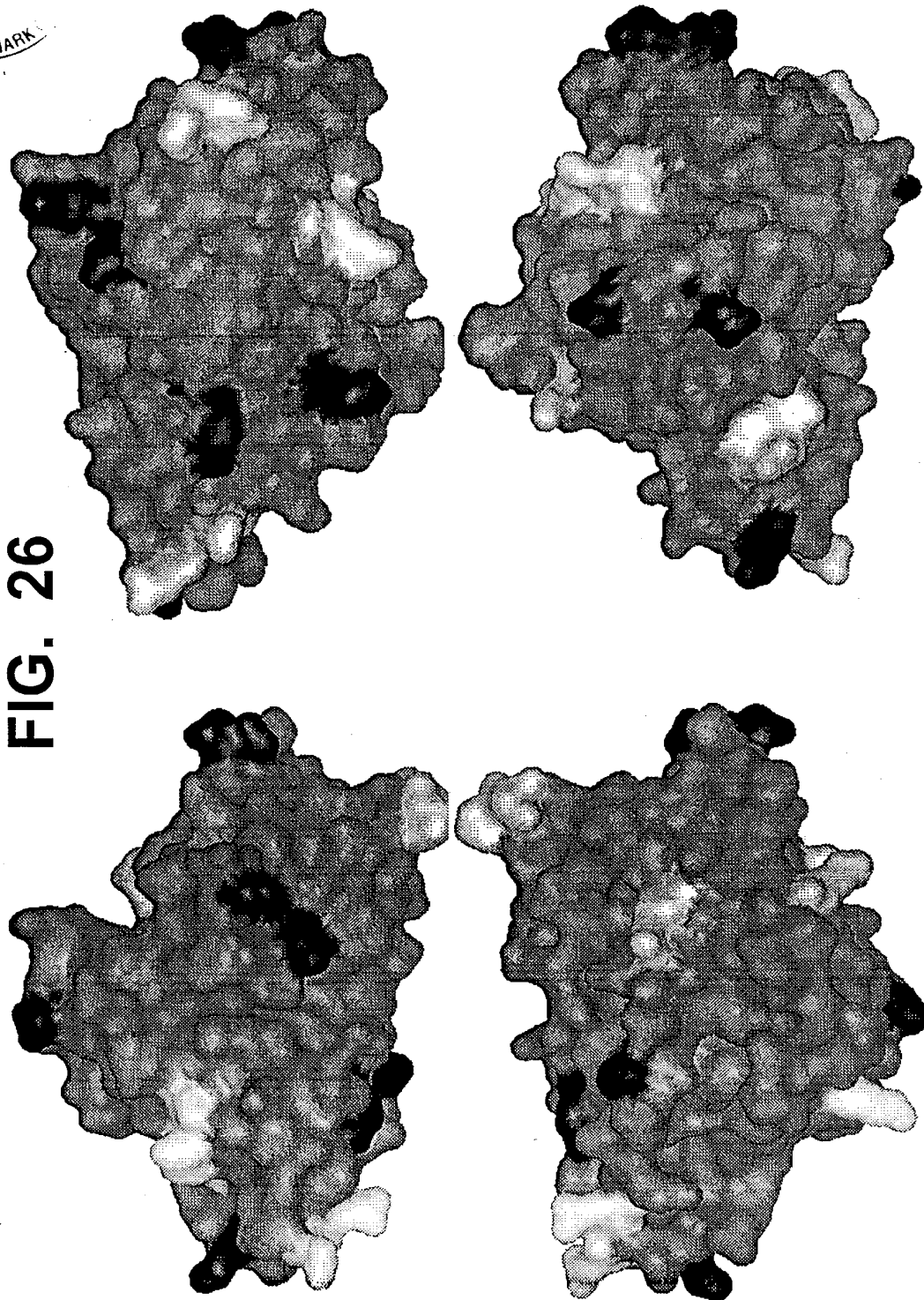
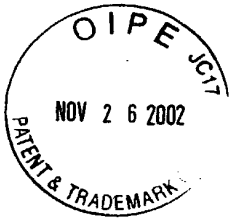


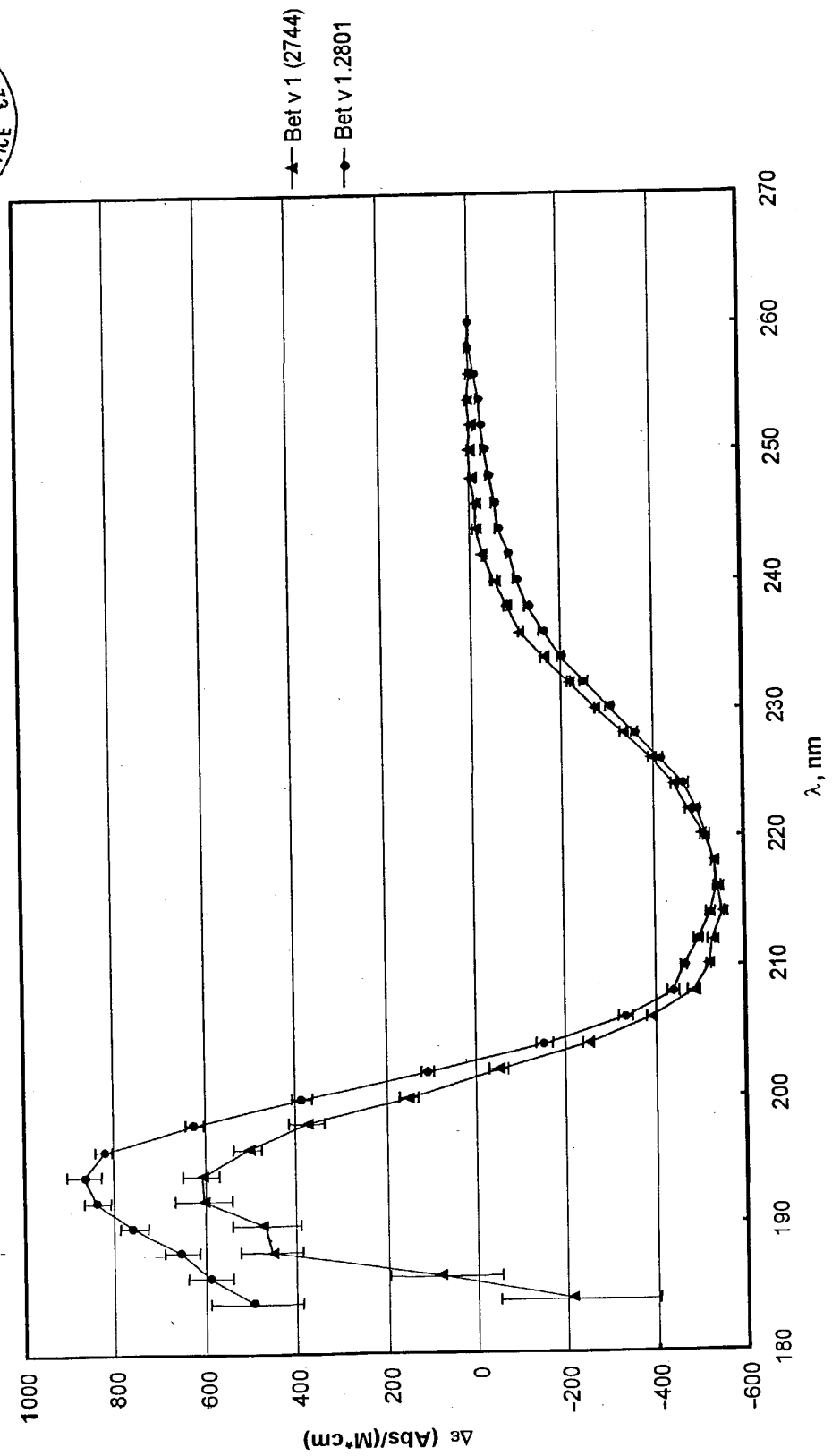
FIG. 26

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FIG. 27



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FIG. 28

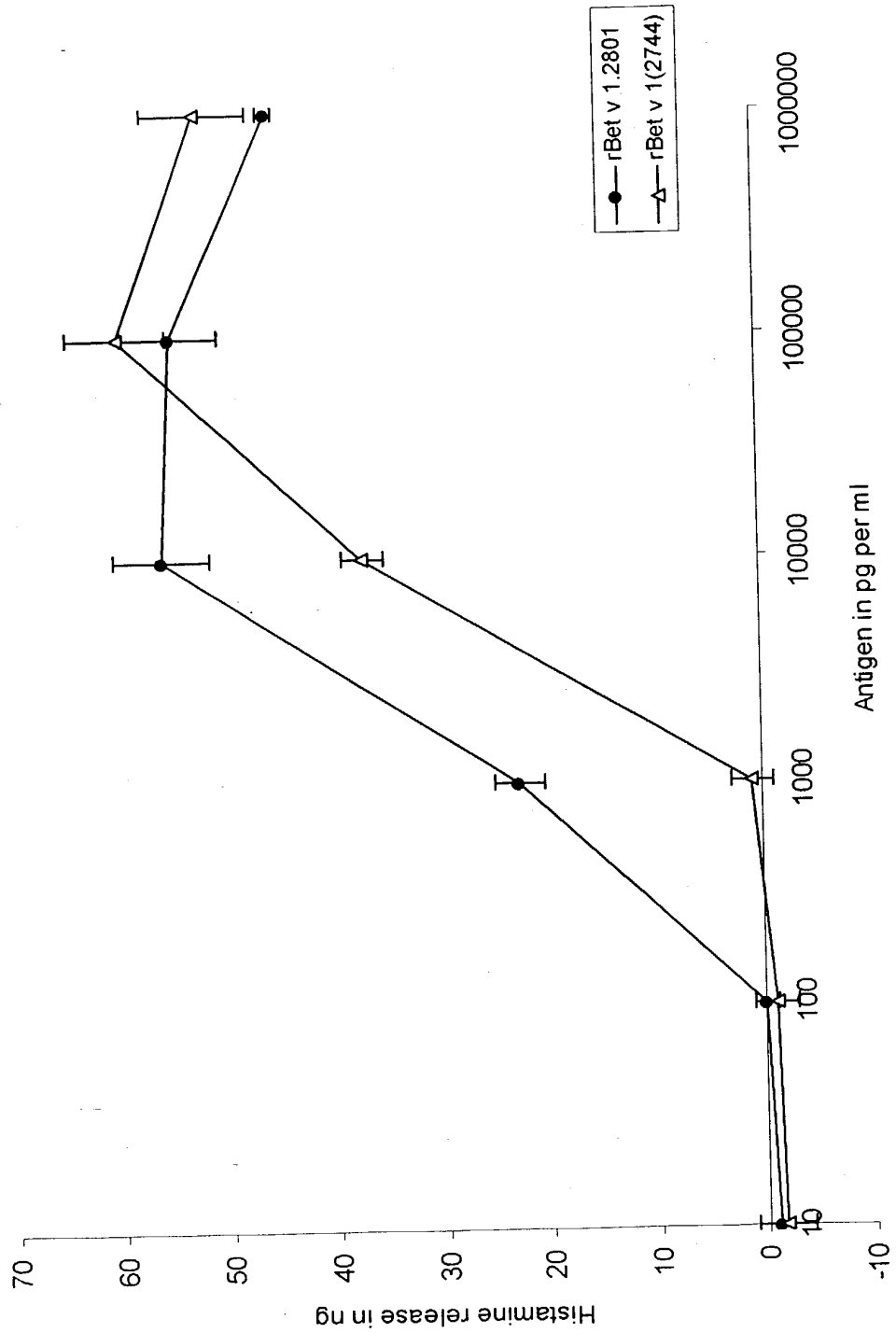




FIG. 29 A

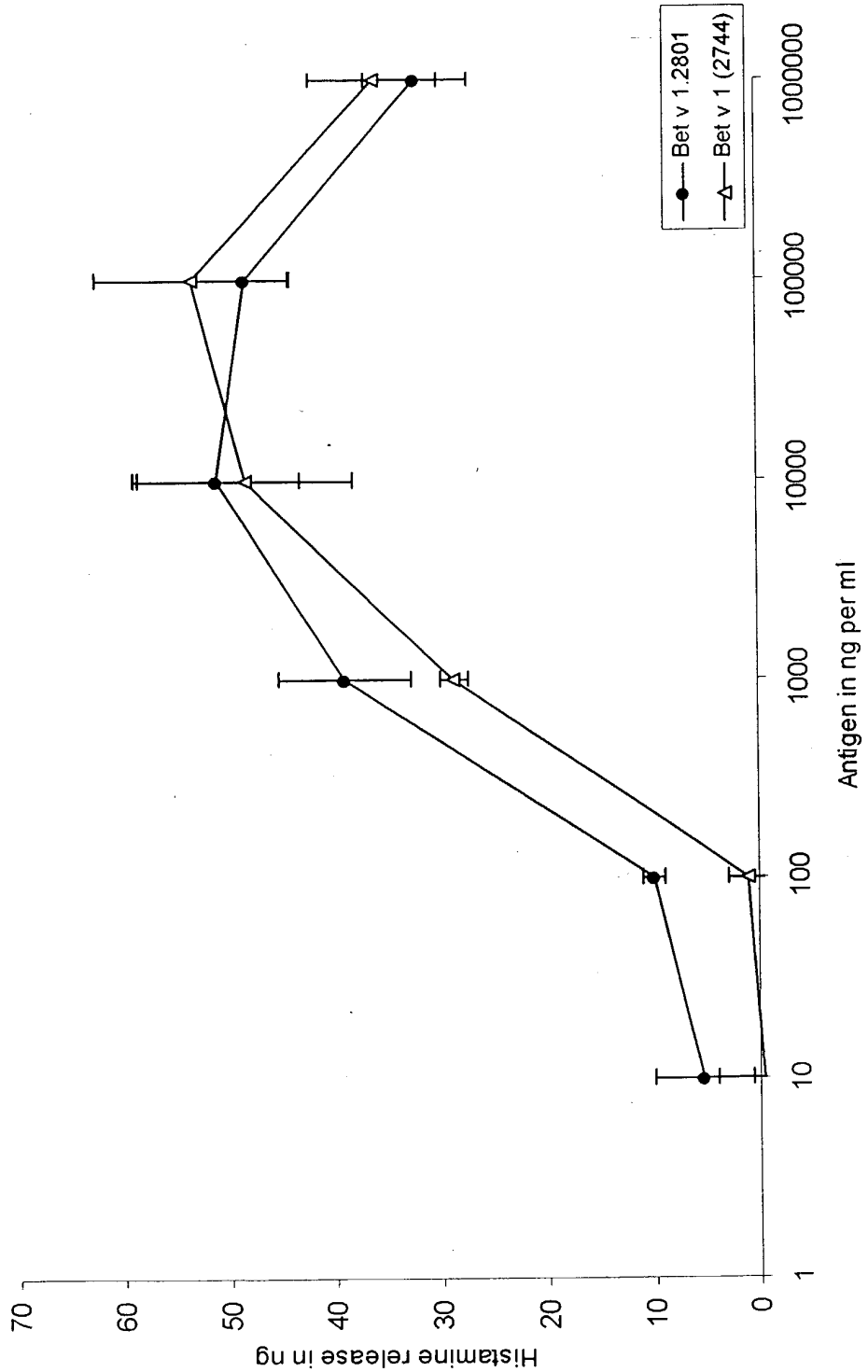
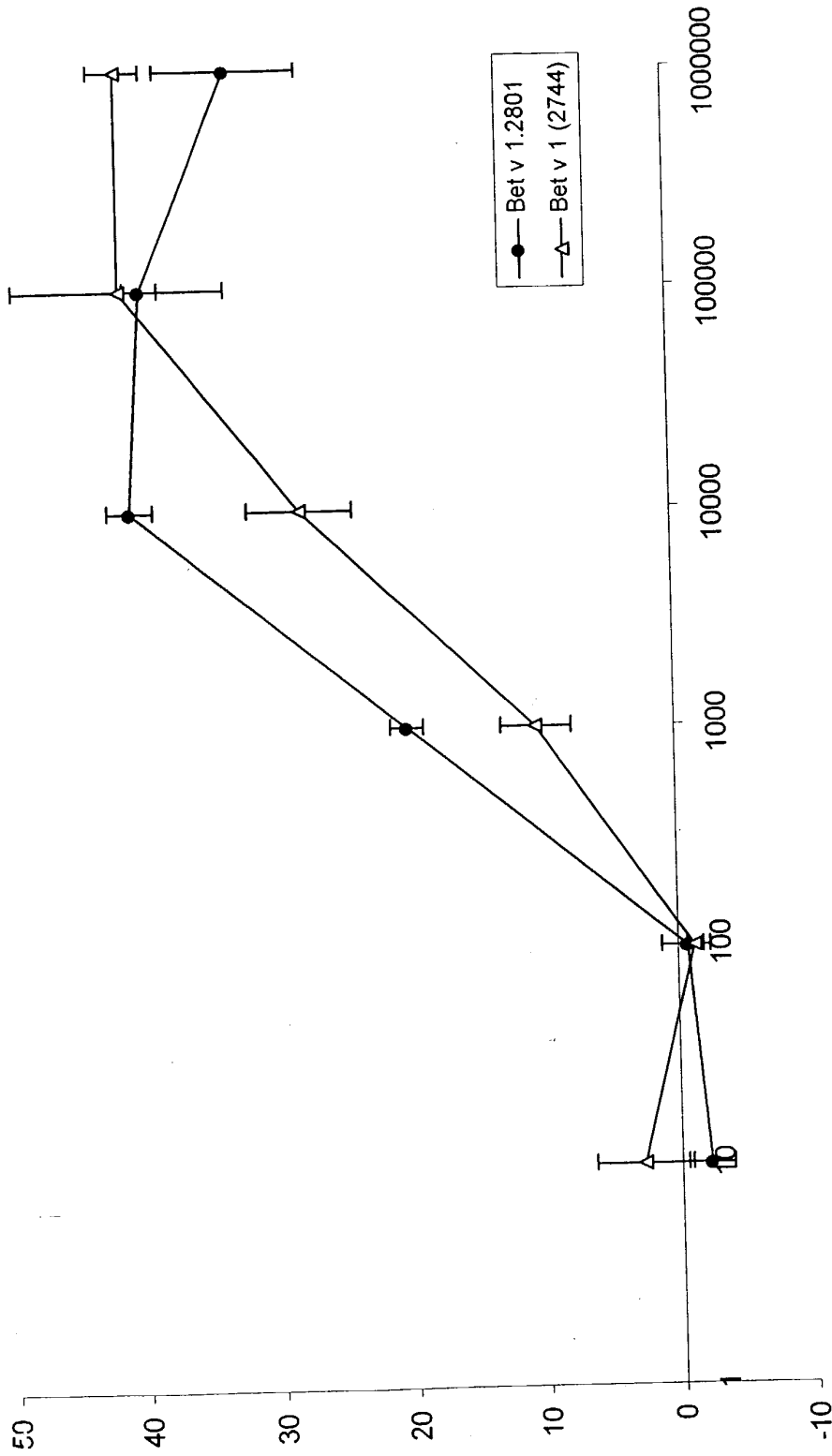




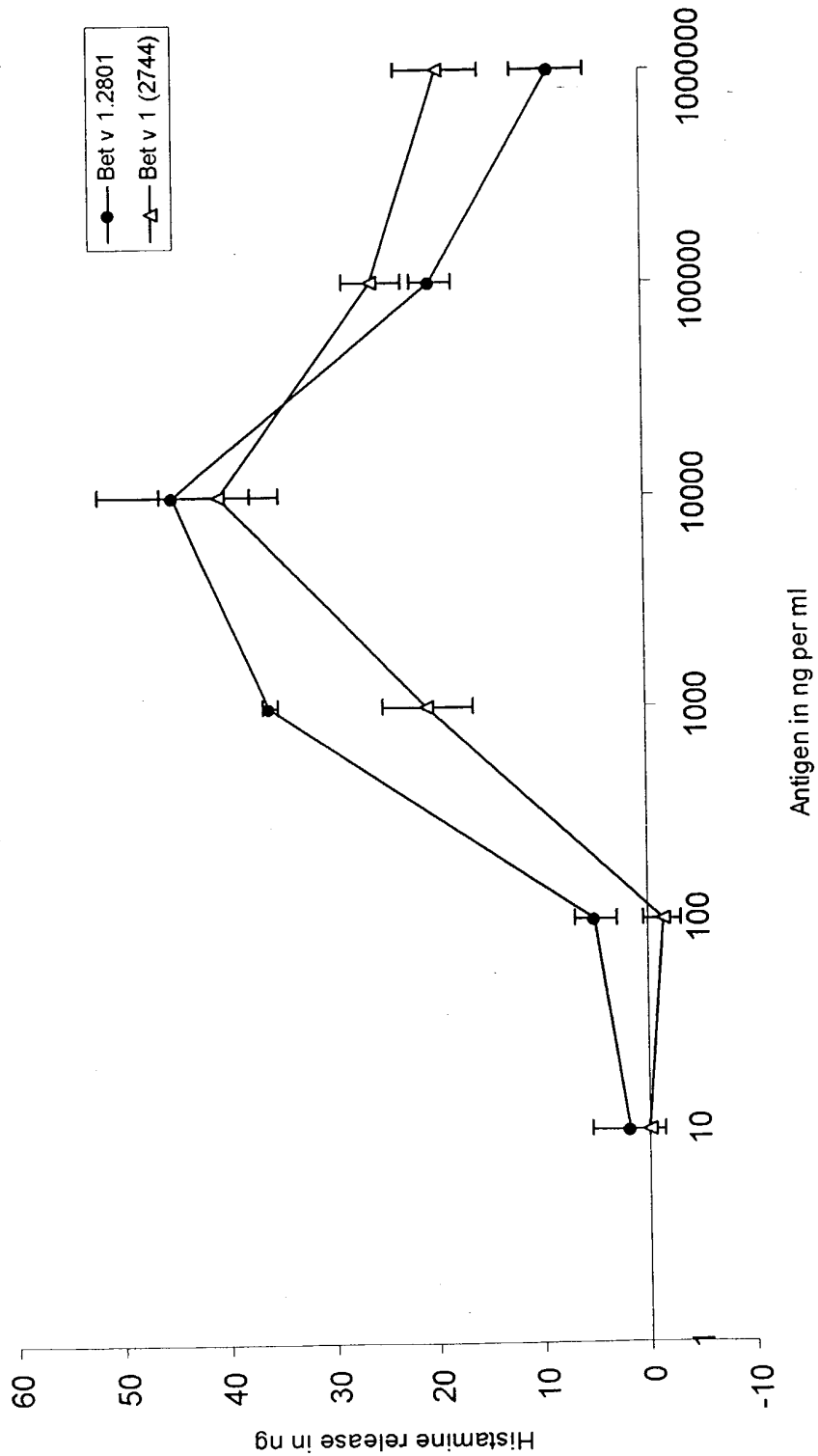
FIG. 29 B



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FIG. 29 C

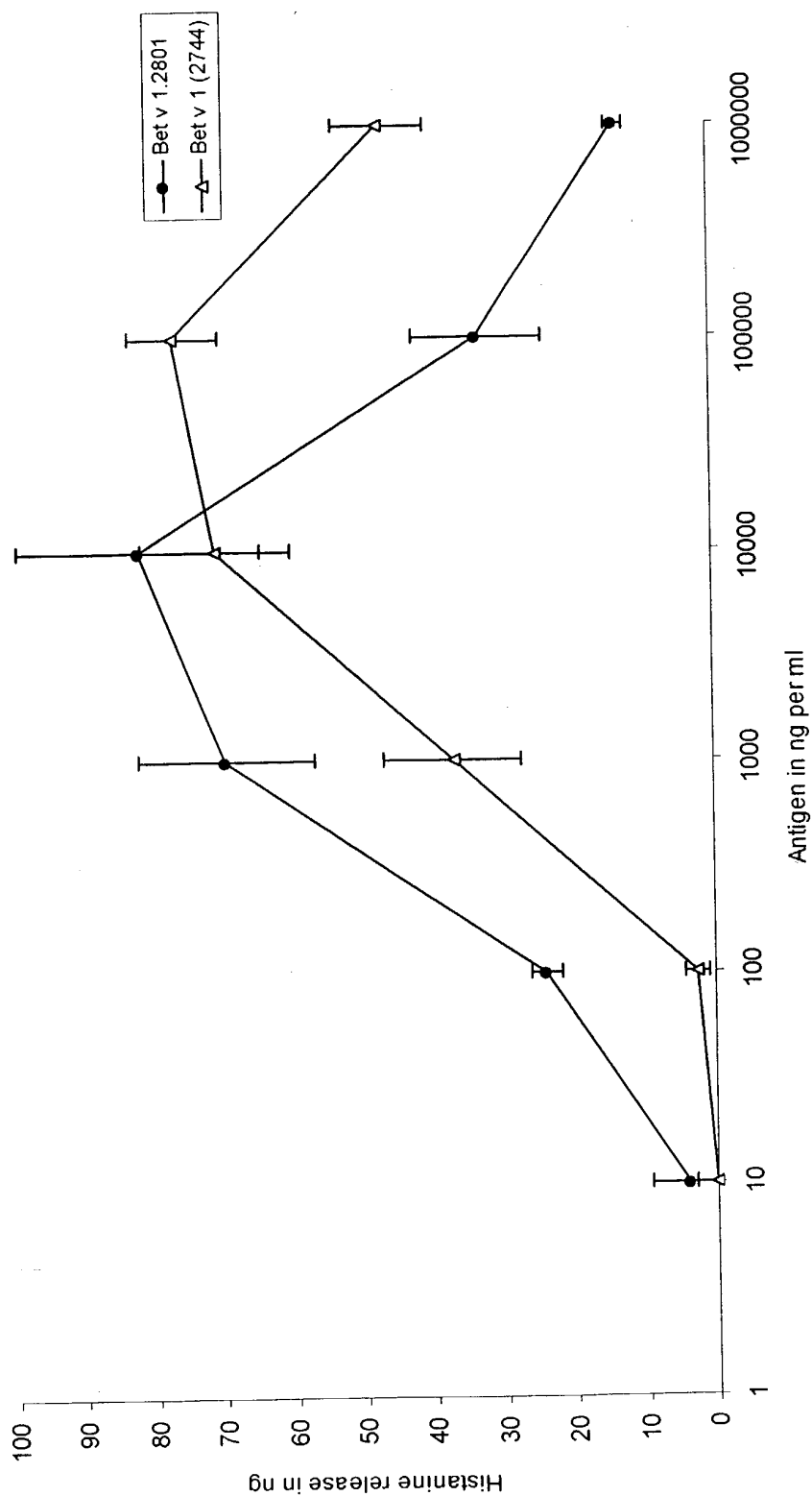




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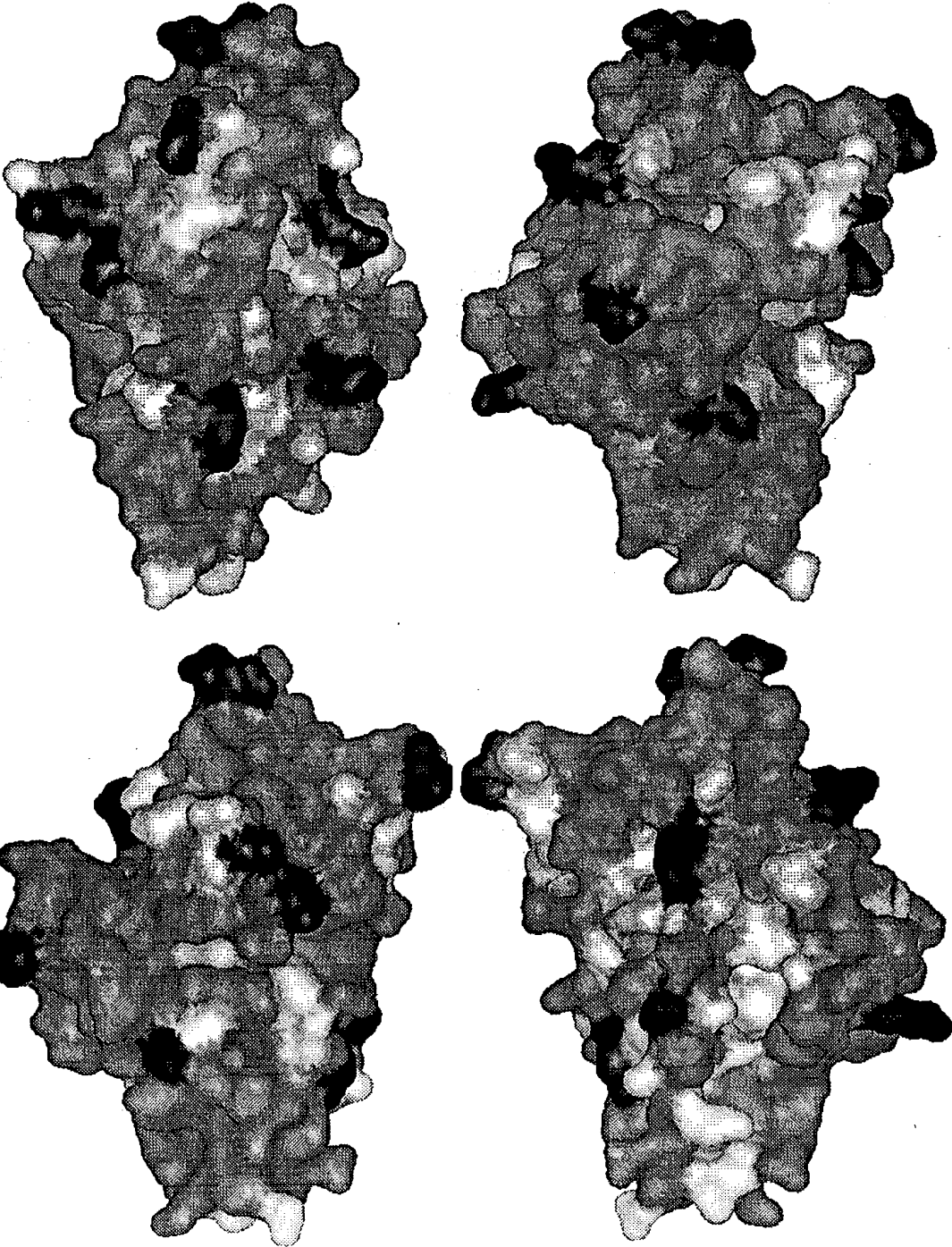
FIG. 29 D



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FIG. 30

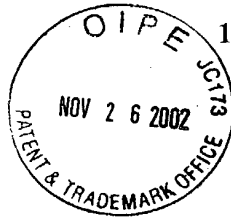


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# FIG. 31

K6A	sense	OB43	42-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCGCCGATTGTGCC- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
K15E	sense	OB44	67-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
H30N	sense	OB46	54-mer	5' -CGGGGTACCAGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC- 3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC- 3'
H74N	sense	OB49	32-mer	5' -CATGGCATGCAATTACATGAAATGCCCATTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
K82N	sense	OB50	50-mer	5' -CTACGCATGCCATTACATGAAATGCCCATTTGGTTAATGGACAA CAATATG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'



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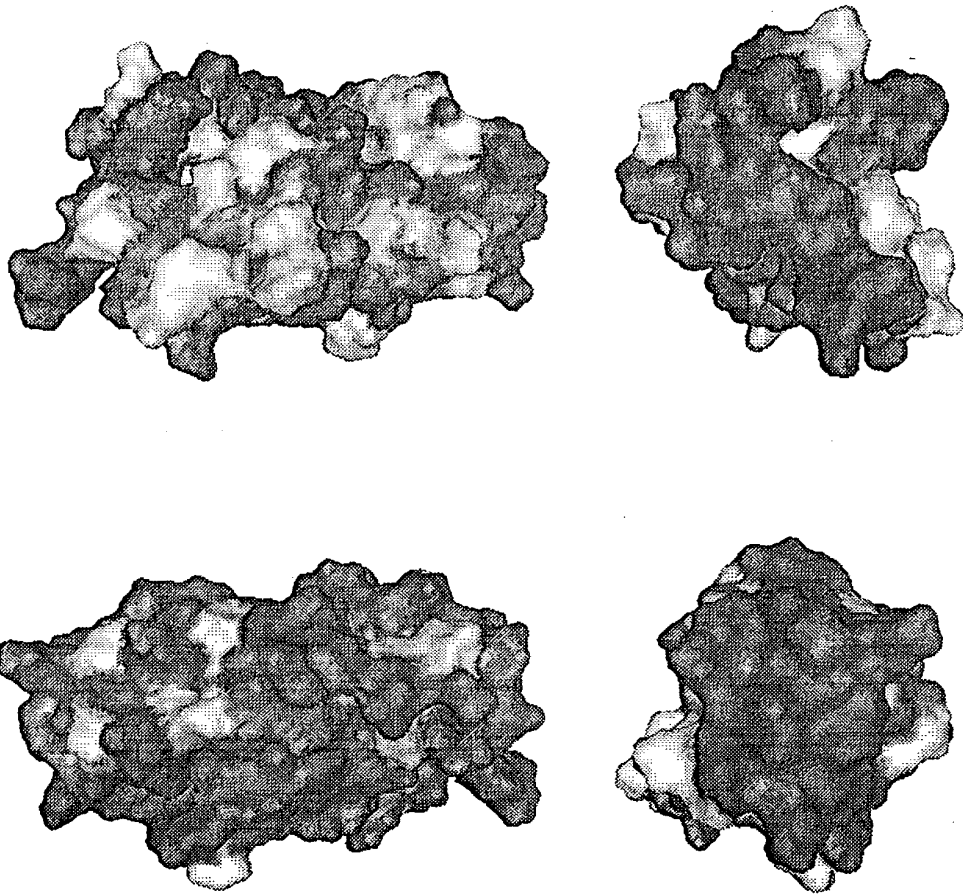
FIG. 32

	1	10	1	10	2	3
1 DERP2-ALK-G Der p2	DQV	VK	DC	AN	HE	IK
2 DERP2-CDNA Der p2	DQV	VK	DC	AN	HE	IK
3 DERP2-ISO101 Der p2	DQV	VK	DC	AN	HE	IK
4 DERP2-ISO102 Der p2	DQV	VK	DC	AN	HE	IK
5 DERP2-ISO104 Der p2	DQV	VK	DC	AN	HE	IK
6 DERP2-ISO113 Der p2	DQV	VK	DC	AN	HE	IK
7 DERP2-ISO120 Der p2	DQV	VK	DC	AN	HE	IK
8 1A9V Der p2	DQV	VK	DC	AN	HE	IK
9 DER2_DERFA Der f2	DQV	VK	DC	AN	HE	IK
10 B61241 Der f2	DQV	VK	DC	AN	HE	IK
11 1AHK Der f2	DQV	VK	DC	AN	HE	IK
12 A61501 Der f2	DQV	VK	DC	AN	HE	IK
13 O96430 Eur m 20101 O96430	DQV	VK	DC	AN	HE	IK
14 O97ZZ Eur m 20102 O97ZZ	DQV	VK	DC	AN	HE	IK
1 DERP2-ALK-G Der p2	DQV	VK	DC	AN	HE	IK
2 DERP2-CDNA Der p2	DQV	VK	DC	AN	HE	IK
3 DERP2-ISO101 Der p2	DQV	VK	DC	AN	HE	IK
4 DERP2-ISO102 Der p2	DQV	VK	DC	AN	HE	IK
5 DERP2-ISO104 Der p2	DQV	VK	DC	AN	HE	IK
6 DERP2-ISO113 Der p2	DQV	VK	DC	AN	HE	IK
7 DERP2-ISO120 Der p2	DQV	VK	DC	AN	HE	IK
8 1A9V Der p2	DQV	VK	DC	AN	HE	IK
9 DER2_DERFA Der f2	DQV	VK	DC	AN	HE	IK
10 B61241 Der f2	DQV	VK	DC	AN	HE	IK
11 1AHK Der f2	DQV	VK	DC	AN	HE	IK
12 A61501 Der f2	DQV	VK	DC	AN	HE	IK
13 O96430 Eur m 20101 O96430	DQV	VK	DC	AN	HE	IK
14 O97ZZ Eur m 20102 O97ZZ	DQV	VK	DC	AN	HE	IK
1 DERP2-ALK-G Der p2	DQV	VK	DC	AN	HE	IK
2 DERP2-CDNA Der p2	DQV	VK	DC	AN	HE	IK
3 DERP2-ISO101 Der p2	DQV	VK	DC	AN	HE	IK
4 DERP2-ISO102 Der p2	DQV	VK	DC	AN	HE	IK
5 DERP2-ISO104 Der p2	DQV	VK	DC	AN	HE	IK
6 DERP2-ISO113 Der p2	DQV	VK	DC	AN	HE	IK
7 DERP2-ISO120 Der p2	DQV	VK	DC	AN	HE	IK
8 1A9V Der p2	DQV	VK	DC	AN	HE	IK
9 DER2_DERFA Der f2	DQV	VK	DC	AN	HE	IK
10 B61241 Der f2	DQV	VK	DC	AN	HE	IK
11 1AHK Der f2	DQV	VK	DC	AN	HE	IK
12 A61501 Der f2	DQV	VK	DC	AN	HE	IK
13 O96430 Eur m 20101 O96430	DQV	VK	DC	AN	HE	IK
14 O97ZZ Eur m 20102 O97ZZ	DQV	VK	DC	AN	HE	IK

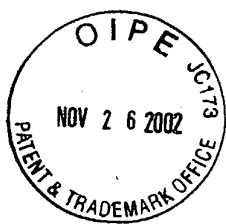
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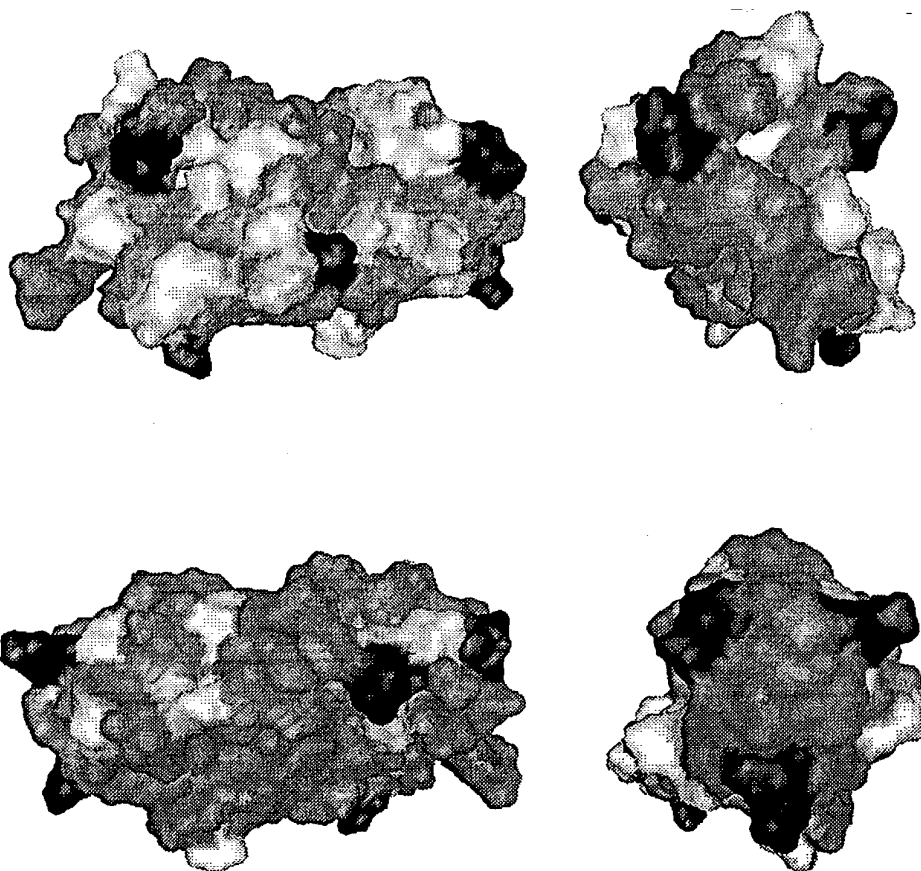
**FIG. 33**



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**FIG. 34**



	1 0 0	9 0	8 0	7 0	6 0	5 0
Derp1 ALK						
Derp1						
Eurm 10101						
Eurm 10101						
Eurm 10102						
Derf1						
Eurm 1						
Derf1						
	4 0	3 0	2 0	1 0	1 0	1 0
Derp1 ALK						
Derp1						
Eurm 10101						
Eurm 10101						
Eurm 10102						
Derf1						
Eurm 1						
Derf1						
	2 0	3 0	4 0	5 0	6 0	7 0
Derp1 ALK						
Derp1						
Eurm 10101						
Eurm 10101						
Eurm 10102						
Derf1						
Eurm 1						
Derf1						

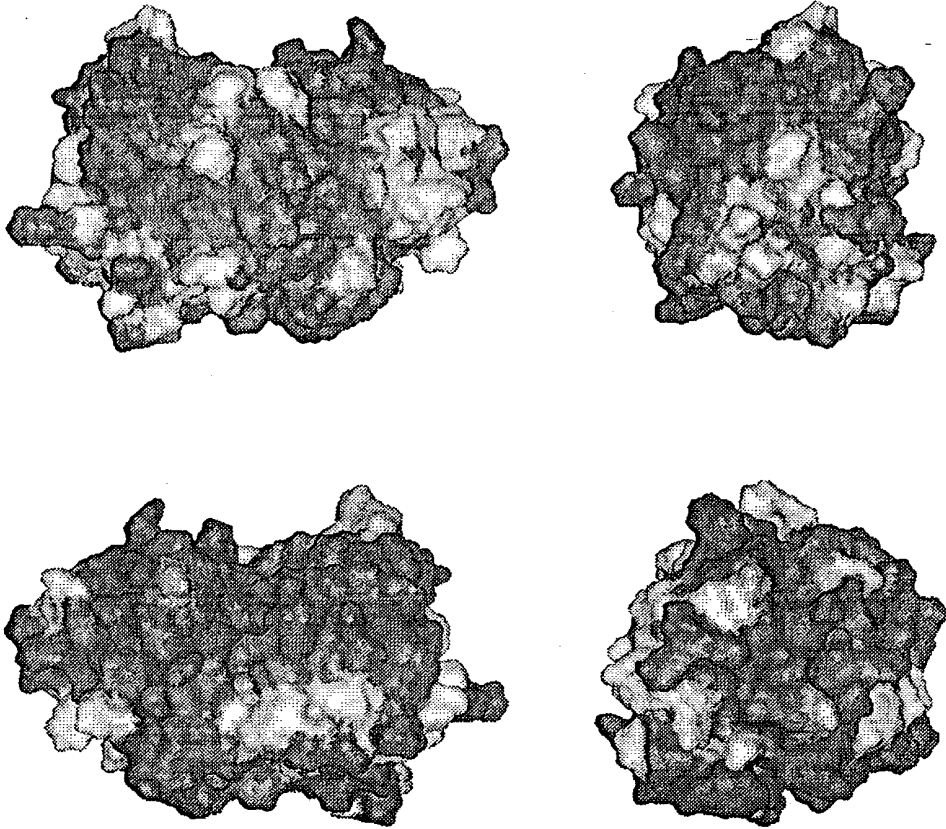
	80	90	100	110	120	130
Derp1 ALK	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H					
Derp1	I P R G I E Y I Q H N G V V Q E S Y Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P H V R K I R E A L A Q T H					
Eurm1 10101	I P R G I E Y I Q Q N G V V Q E H Y Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S N K I R Q A L T Q T H					
Eurm1 10101	I P R G I E Y I Q Q N G V V Q E H Y Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S N K I R Q A L T Q T H					
Eurm1 10102	I P R G I E Y I Q Q N G V V Q E H Y Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S N K I R Q A L T Q T H					
Derf1	I P R G I E Y I Q Q N G V V Q E H Y Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S N K I R Q A L T Q T H					
Eurm1	I P R G I E Y I Q Q N G V V Q E H Y Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S N K I R Q A L T Q T H					
Derf1	I P R G I E Y I Q Q N G V V Q E H Y Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S N K I R Q A L T Q T H					
	140	150	160	170	180	190
Derp1 ALK	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P P N Y H A V N I V G Y S N A Q G V D Y W I V R N S W D T N					
Derp1	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P P N Y H A V N I V G Y S N A Q G V D Y W I V R N S W D T N					
Eurm1 10101	T A V A V I I G I K D L N A F R H Y D G R T I M Q H D N G Y Q P P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
Eurm1 10101	T A V A V I I G I K D L N A F R H Y D G R T I M Q H D N G Y Q P P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
Eurm1 10102	T A V A V I I G I K D L N A F R H Y D G R T I M Q H D N G Y Q P P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
Derf1	T A V A V I I G I K D L N A F R H Y D G R T I M Q H D N G Y Q P P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
Eurm1	T A V A V I I G I K D L N A F R H Y D G R T I M Q H D N G Y Q P P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
Derf1	T A V A V I I G I K D L N A F R H Y D G R T I M Q H D N G Y Q P P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T					
	200	210	220			
Derp1 ALK	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L					
Derp1	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L					
Eurm1 10101	W G D N G Y G Y F A A N I N L M M I E Q Y P Y V V M L					
Eurm1 10101	W G D N G Y G Y F A A N I N L M M I E Q Y P Y V V M L					
Eurm1 10102	W G D N G Y G Y F A A N I N L M M I E Q Y P Y V V I L					
Derf1	W G D S G Y G Y F A A N I N L M M I E Q Y P Y V V I M					
Eurm1	W G D N G Y G Y F A A N I N L M M I E Q Y P Y V V I L					
Derf1	W G D S G Y G Y F A A N I N L M M I E Q Y P Y V V I L					



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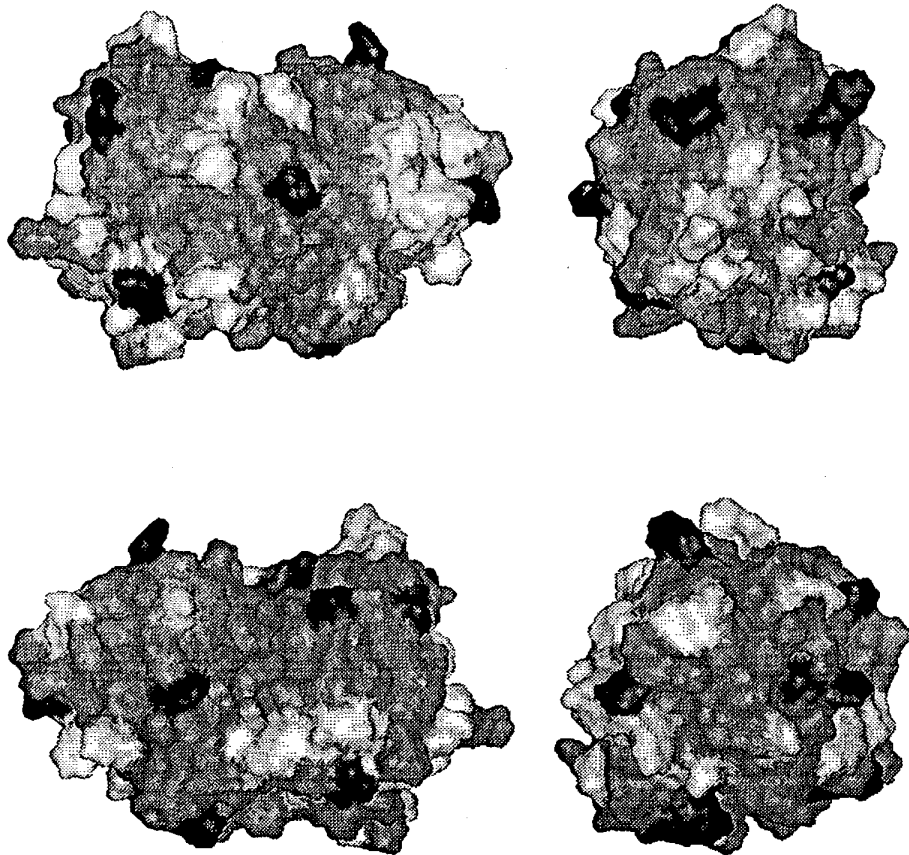
**FIG. 36**



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**FIG. 37**



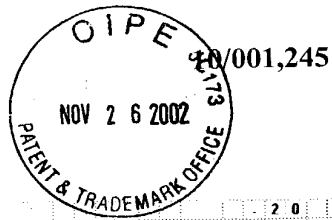
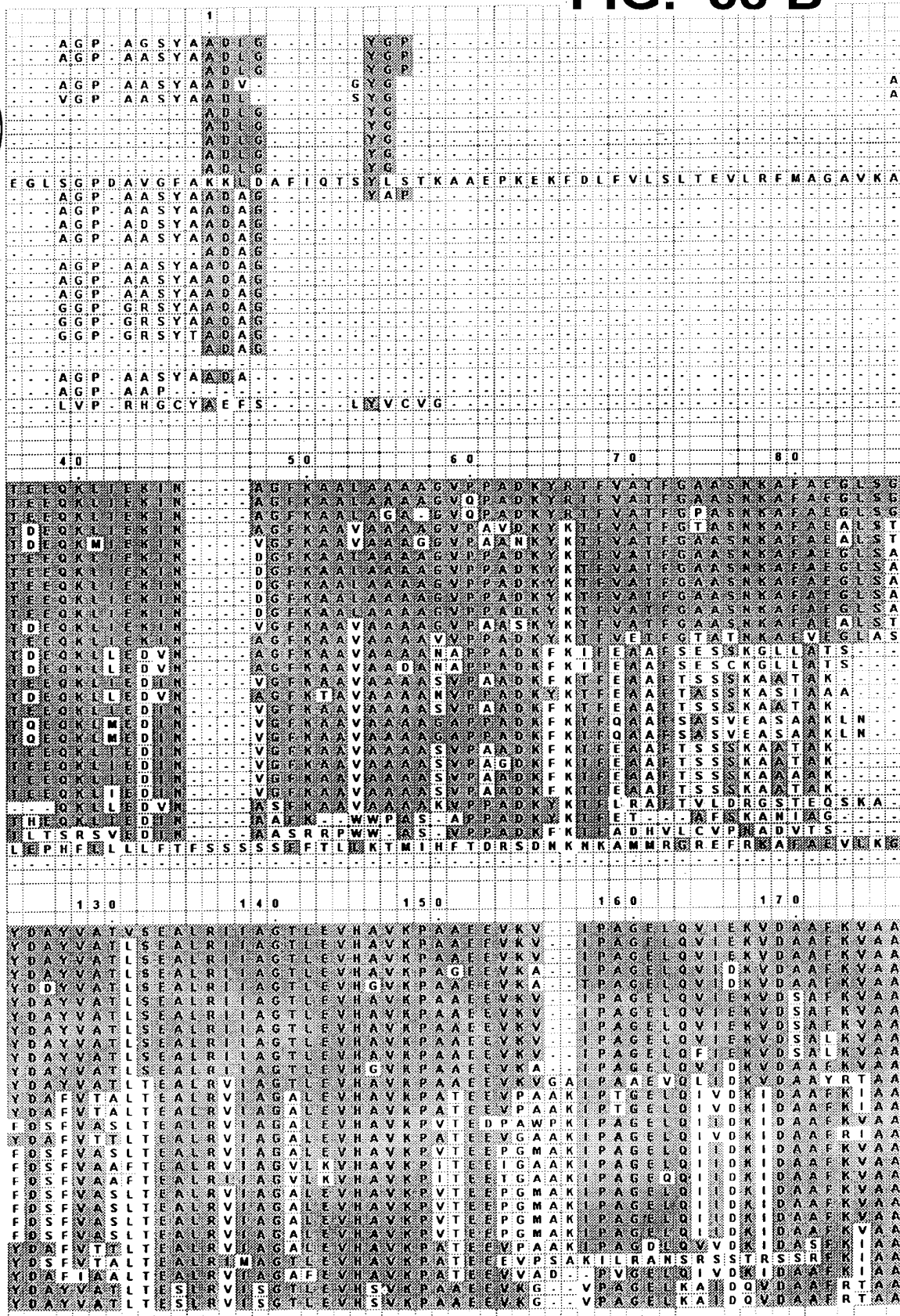


FIG. 38 A

		20	10	
trj081341j081341	Phl p 5.0103	MAVHQYTVLFLAVALV		
trj040960j040960	Phl p 5	MAVHQYTVLFLAVALV		
spj040962jMP5A_PHLPR	Phl p 5 A	MAVHQYTVLFLAVALV		
spjP22265jMP92_POAPR	Poa p 5 (KBG41)	MAVHQYTVLFLAVALV		
spjP22266jMP93_POAPR	Poa p 5 (KBG60)	MAVQKYTVLFLAVALV		
trj065319j065319	Phl p 5			
trj065320j065320	Phl p 5			
trj065321j065321	Phl p 5			
trj065318j065318	Phl p 5			
trjP93467jP93467	Phl p 5			
spjP22264jMP91_POAPR	Poa p 5 (KBG 31)	MDKANGAYKTALKAASAVAPAEKFPVFOATFDKNLK		
spj040237jMP5B_LOLPR	Lol p 5B	MAVQKHTVALFLAVALV		
trj09XF24j09XF24	Lol p 5A	MAVQKHTVALFLAVALV		
trj09SC99j09SC99	Lol p 5C	MAVQKHTVALFLAVALV		
trj081343j081343	Phl p 5.0206	MAVQKHTVALFLAVALV		
trj023972j023972	Hol I 5			
trj081344j081344	Phl p 5.0207	MAVQKHTVALFLAVALV		
trjAAG42255jAAG42255	Hol I 5B	MAVQKHTVALFLAVALV		
trjAAG42254jAAG42254	Poa p 5	MAVQKHTVALFLAVALV		
trj081342j081342	Phl p 5.0203	SVKRSNGSAEVHRAVPRRRGPR		
trjP93466jP93466	Phl p 5	AAAVPRRRGPR		
spj040963jMP5B_PHLPR	Phl p 5B			
trj09SBE0j09SBE0	Phl p 5.0204			
trj023971j023971	Phl p 5.02			
spjP56166jMP53_PHAHQ	Pha a 5.3	MAVQKHTVALFLAVALV		
HAHQ	Pha a 5.1	MAVQKHTVALFLAVALV		
trj004828j004828	Hor v 9	MAVQKHTVALFLAVALV		
trjQ39995jQ39995	Hor v 5 (30kDa)	MAVQKHTVALFLAVALV		
		10	20	30
trj081341j081341	Phl p 5.0103	ATPAAAPAGYTPATPAAPAG		ALPAGKAT
trj040960j040960	Phl p 5	ATPAAAPAGYTPATPAAPAG		ALPAGKAT
spj040962jMP5A_PHLPR	Phl p 5 A	ATPAAAPAGYTPATPAAPAG		ADAGKAT
spjP22265jMP92_POAPR	Poa p 5 (KBG41)	PATLAPATPAAGYTPATPAAPAG		ADAGKAT
spjP22266jMP93_POAPR	Poa p 5 (KBG60)	PATLAPATPAAGYTPATPAAPAG		ADAGKAT
trj065319j065319	Phl p 5	GATPAAPAG		ADAGKAT
trj065320j065320	Phl p 5	GATPAAPAG		ADAGKAT
trj065321j065321	Phl p 5	GATPAAPAG		ADAGKAT
trj065318j065318	Phl p 5	GATPAAPAG		ADAGKAT
trjP93467jP93467	Phl p 5	GATPAAPAG		ADAGKAT
spjP22264jMP91_POAPR	Poa p 5 (KBG 31)	PASKFPAPKAPKVAAYTPATPAAPAG		ADAGKAT
spj040237jMP5B_LOLPR	Lol p 5B	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj09XF24j09XF24	Lol p 5A	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj09SC99j09SC99	Lol p 5C	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj081343j081343	Phl p 5.0206	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj023972j023972	Hol I 5	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj081344j081344	Phl p 5.0207	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trjAAG42255jAAG42255	Hol I 5B	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trjAAG42254jAAG42254	Poa p 5	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj081342j081342	Phl p 5.0203	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trjP93466jP93466	Phl p 5	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
spj040963jMP5B_PHLPR	Phl p 5B	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj09SBE0j09SBE0	Phl p 5.0204	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj023971j023971	Phl p 5.02	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
spjP56166jMP53_PHAHQ	Pha a 5.3	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
HAHQ	Pha a 5.1	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trj004828j004828	Hor v 9	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
trjQ39995jQ39995	Hor v 5 (30kDa)	ATPATPAAPATAATPATPATPAAPAG		ADAGKAT
		90	100	110
trj081341j081341	Phl p 5.0103	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj040960j040960	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spj040962jMP5A_PHLPR	Phl p 5 A	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spjP22265jMP92_POAPR	Poa p 5 (KBG41)	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spjP22266jMP93_POAPR	Poa p 5 (KBG60)	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj065319j065319	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj065320j065320	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj065321j065321	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj065318j065318	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjP93467jP93467	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spjP22264jMP91_POAPR	Poa p 5 (KBG 31)	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spj040237jMP5B_LOLPR	Lol p 5B	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj09XF24j09XF24	Lol p 5A	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj09SC99j09SC99	Lol p 5C	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj081343j081343	Phl p 5.0206	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj023972j023972	Hol I 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj081344j081344	Phl p 5.0207	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjAAG42255jAAG42255	Hol I 5B	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjAAG42254jAAG42254	Poa p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj081342j081342	Phl p 5.0203	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjP93466jP93466	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spj040963jMP5B_PHLPR	Phl p 5B	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj09SBE0j09SBE0	Phl p 5.0204	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj023971j023971	Phl p 5.02	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spjP56166jMP53_PHAHQ	Pha a 5.3	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
HAHQ	Pha a 5.1	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj004828j004828	Hor v 9	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjQ39995jQ39995	Hor v 5 (30kDa)	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
		120		
trj081341j081341	Phl p 5.0103	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj040960j040960	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spj040962jMP5A_PHLPR	Phl p 5 A	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spjP22265jMP92_POAPR	Poa p 5 (KBG41)	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spjP22266jMP93_POAPR	Poa p 5 (KBG60)	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj065319j065319	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj065320j065320	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj065321j065321	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj065318j065318	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjP93467jP93467	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spjP22264jMP91_POAPR	Poa p 5 (KBG 31)	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spj040237jMP5B_LOLPR	Lol p 5B	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj09XF24j09XF24	Lol p 5A	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj09SC99j09SC99	Lol p 5C	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj081343j081343	Phl p 5.0206	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj023972j023972	Hol I 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj081344j081344	Phl p 5.0207	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjAAG42255jAAG42255	Hol I 5B	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjAAG42254jAAG42254	Poa p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj081342j081342	Phl p 5.0203	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjP93466jP93466	Phl p 5	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spj040963jMP5B_PHLPR	Phl p 5B	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj09SBE0j09SBE0	Phl p 5.0204	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj023971j023971	Phl p 5.02	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
spjP56166jMP53_PHAHQ	Pha a 5.3	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
HAHQ	Pha a 5.1	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trj004828j004828	Hor v 9	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		
trjQ39995jQ39995	Hor v 5 (30kDa)	EPKKGAAESSSKAALTSKLDAAAYKLAYKTAEAGATPEAKK		

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**FIG. 38 B**

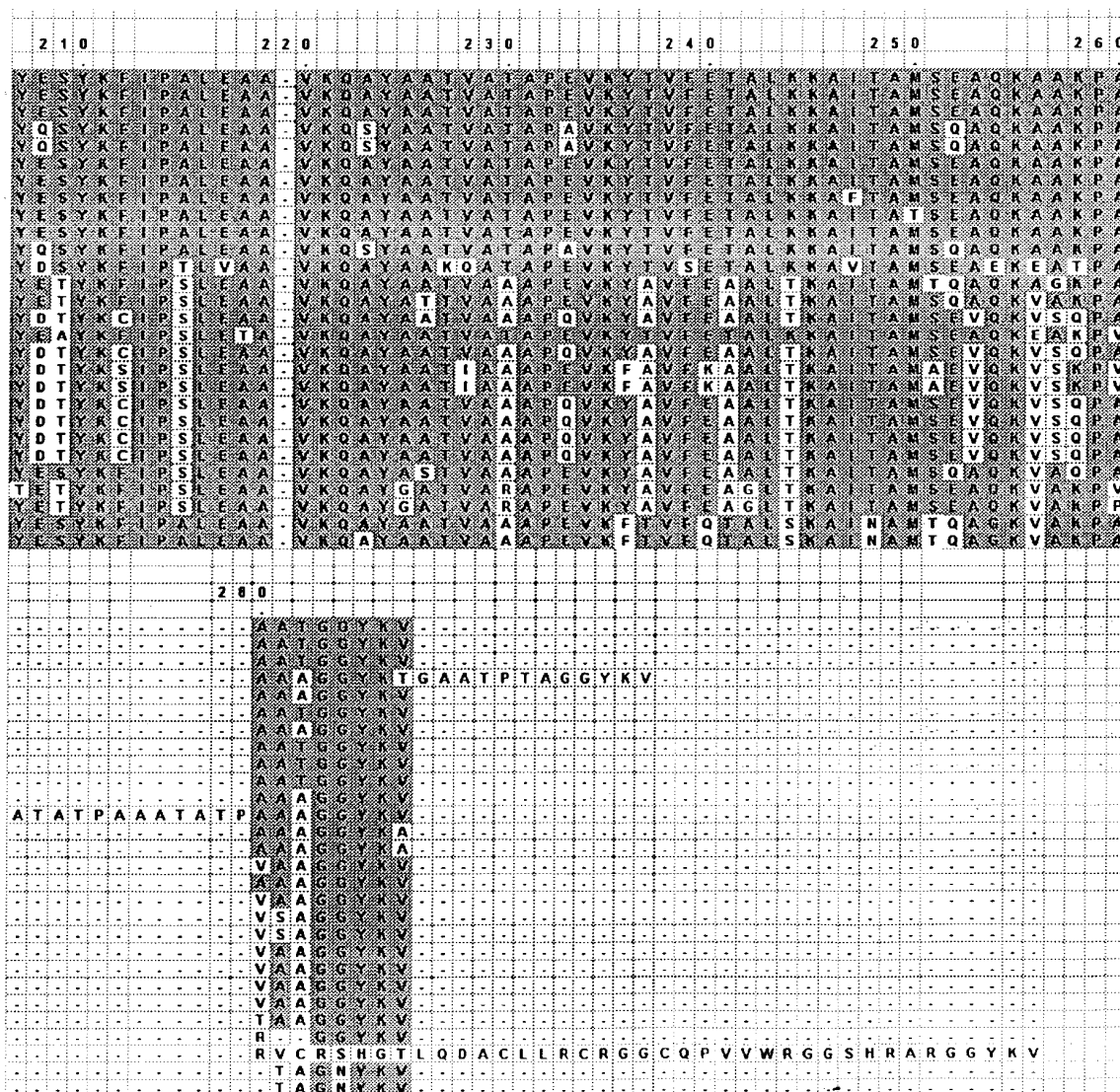


[illegible]

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**FIG. 38 D**

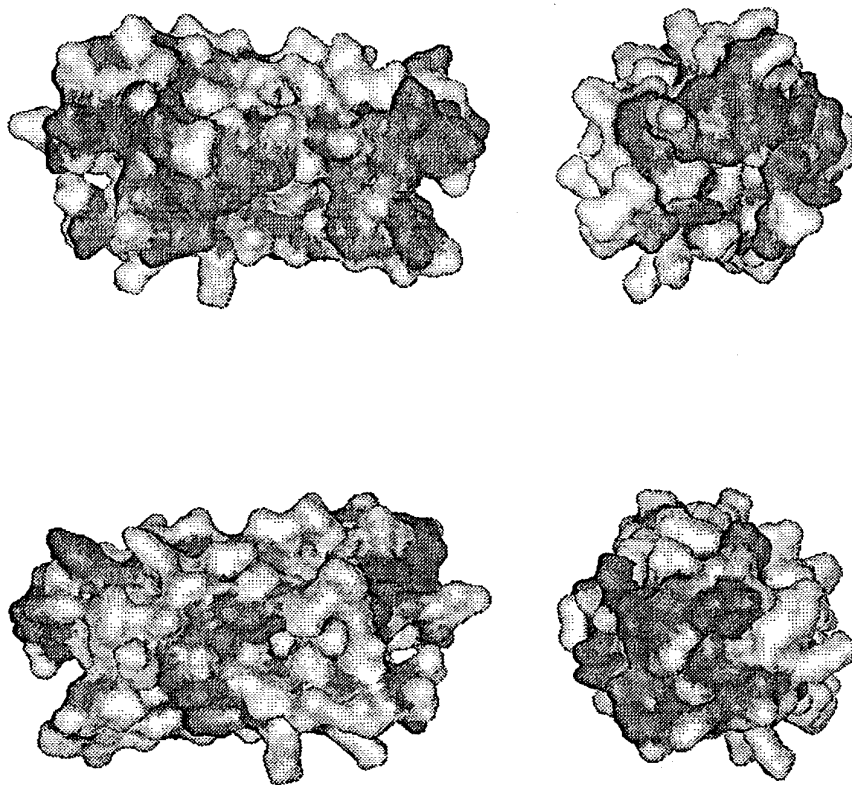




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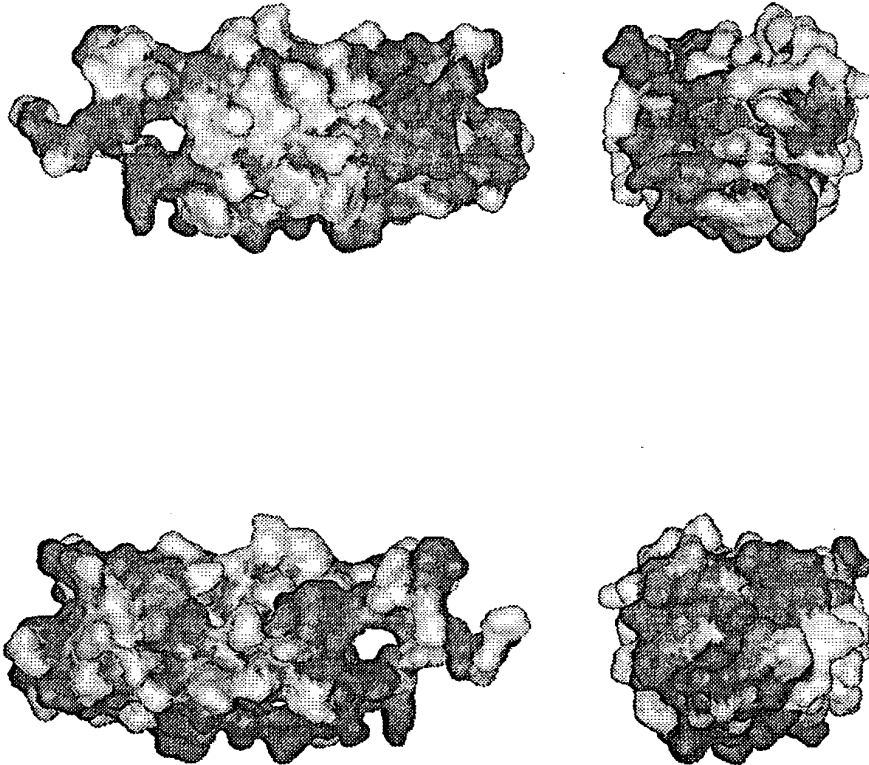
**FIG. 39 A**



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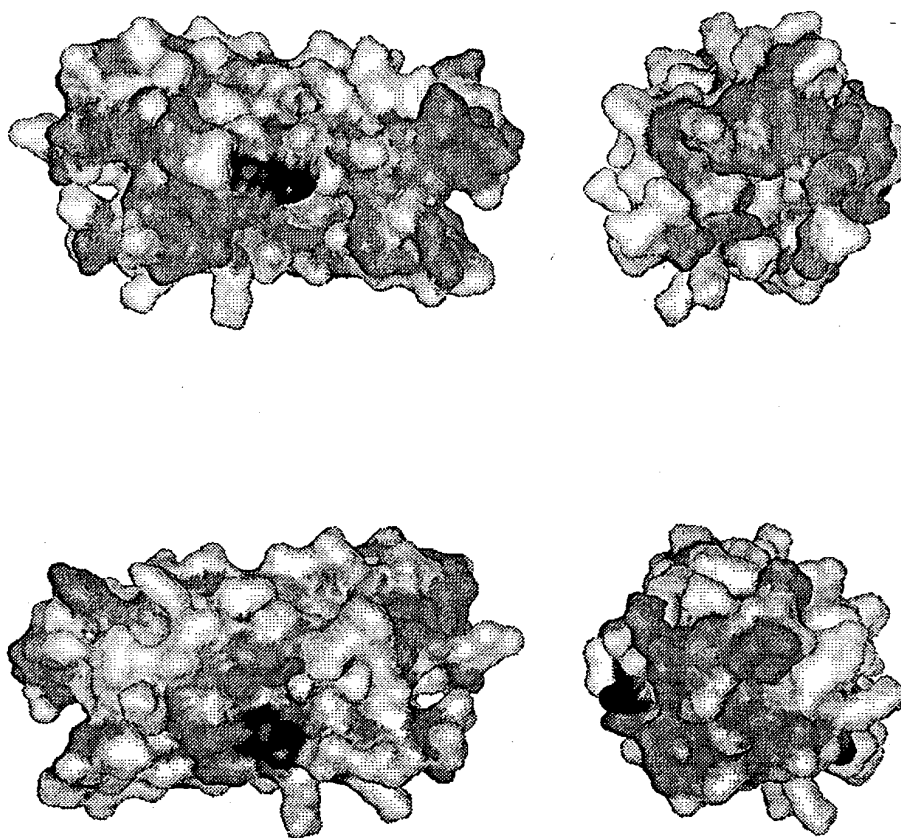


**FIG. 39 B**





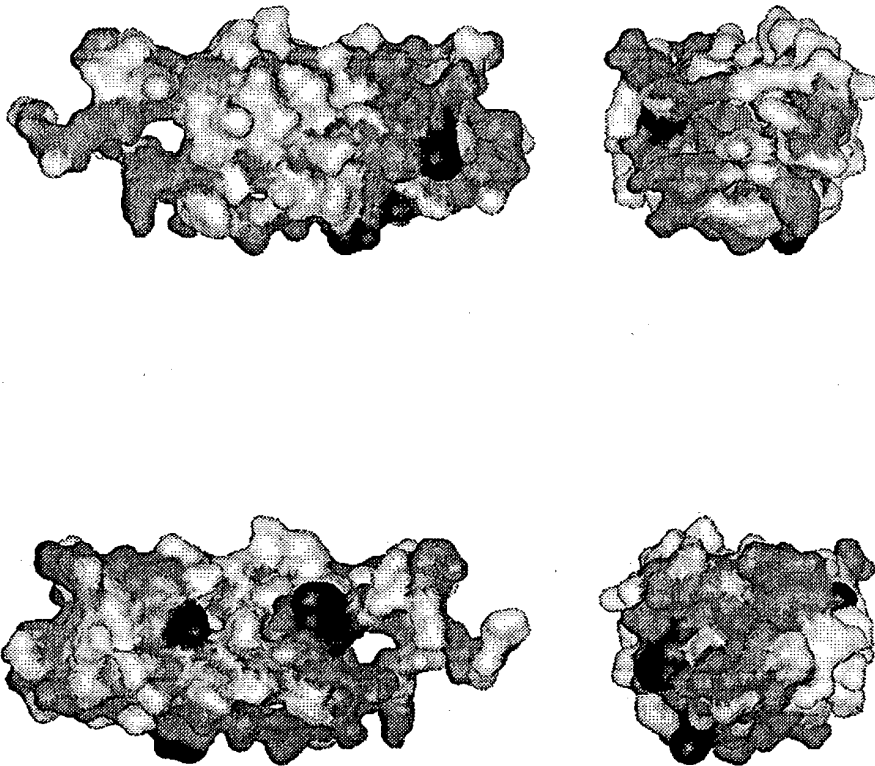
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**FIG. 40 A**

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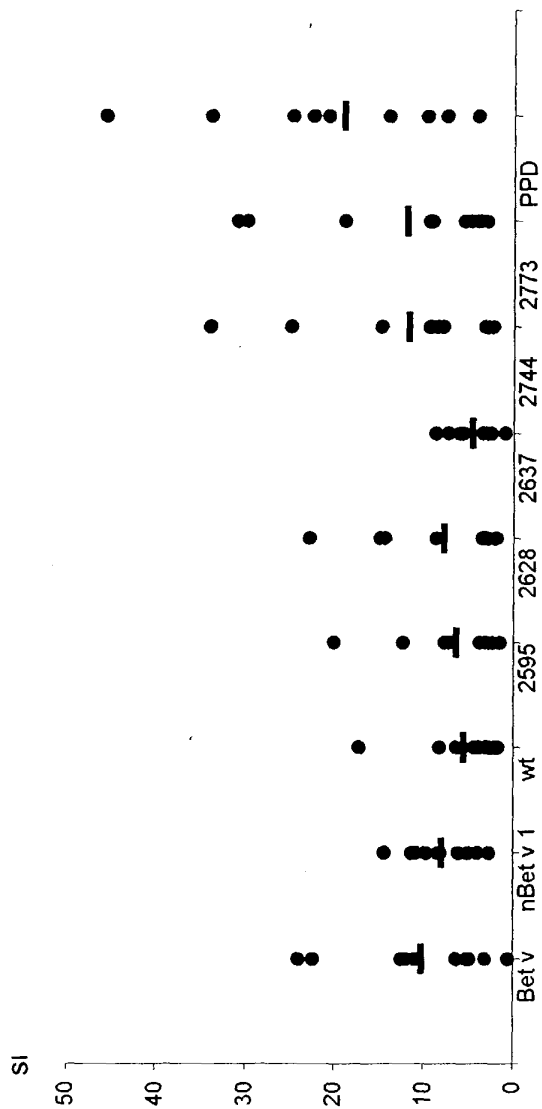
**FIG. 40 B**



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FIG. 41



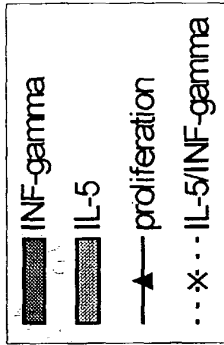
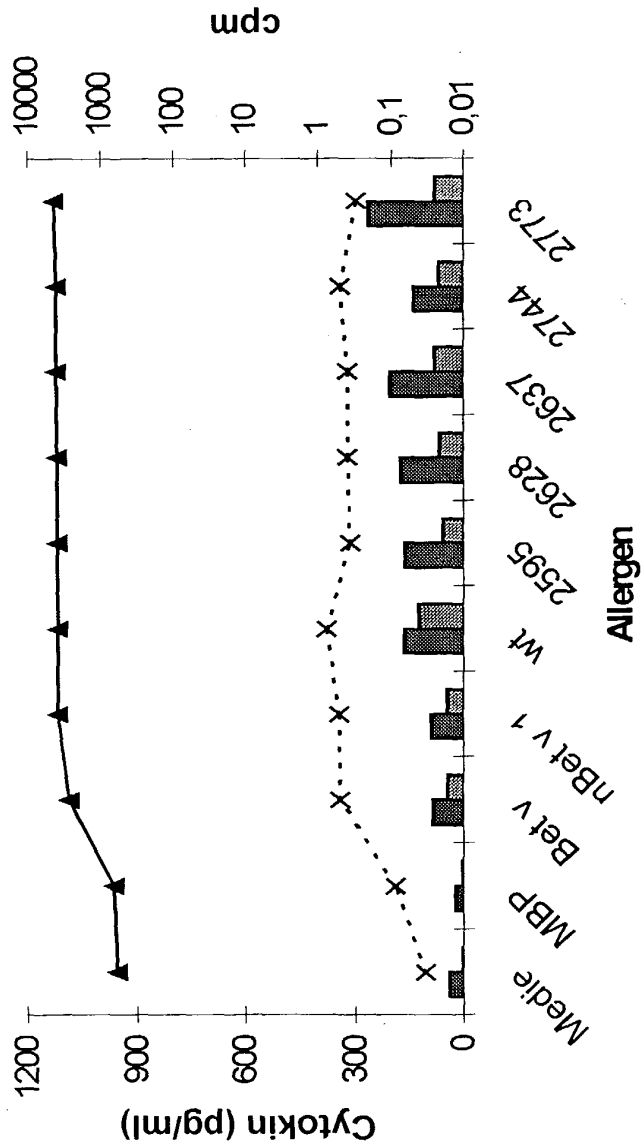


FIG. 42



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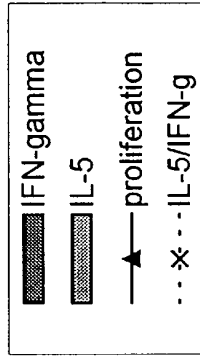
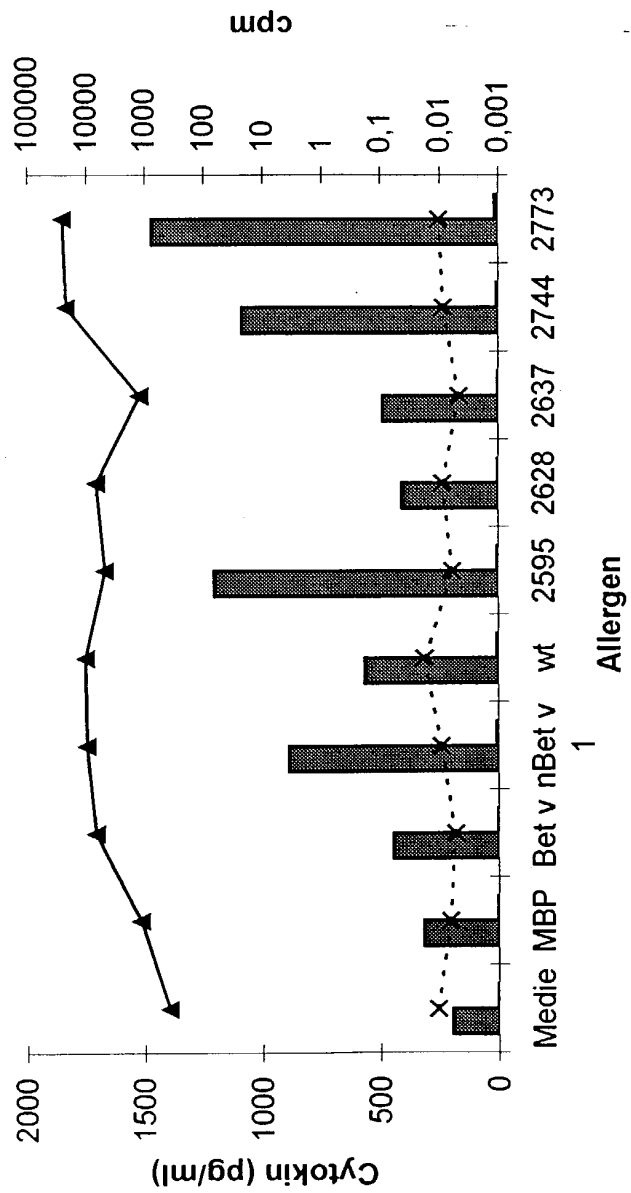


FIG. 43





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FIG. 44

